

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sun Aug 8 17:01:38 1999; MasPar time 13516.58 Seconds
Tabular output not generated. 1569.436 Million cell updates/sec

Title: >US-08-287-669-18
Description: (1-7653) from US08287669.seq (10 of 10)
Perfect Score: 7653
N.A. Sequence: 1 AGATCTGAATAAGGTGATA.....ATTCTGGTCAGCAAGATCT 7653
Comp: TCTAGACTTTATTCCTACTAT.....TAAGACCAGTCGTTCTAGA

Scoring table: TABLE jmetric
Gap 60

Nmatch STD : Dbase 0; Query 0

Searched: 646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database: emb158
1:em_bal 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
genbank111
17:gb_bal 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vi

Statistics: Mean 10.846; Variance 5.255; scale 2.064

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	7653	100.0	7653	21	CELCED3A		Caenorhabditis elegans	0.00e+00
2	4164	54.4	39908	21	CEC48D1		Caenorhabditis elegans	0.00e+00
3	3359	43.9	314495	19	CEY67H2		Caenorhabditis elegans	0.00e+00
4	73	1.0	224746	19	CEY56A3		Caenorhabditis elegans	1.25e-33
5	71	0.9	4917	19	AC006766		Caenorhabditis elegans	4.31e-32
6	71	0.9	4917	22	CELY44E3B		Caenorhabditis elegans	4.31e-32
7	72	0.9	38846	19	AC006696		Caenorhabditis elegans	7.36e-33
8	69	0.9	42724	21	CEY53A2		Caenorhabditis elegans	1.46e-30
9	72	0.9	43152	21	CELF59B1		Caenorhabditis elegans	7.36e-33
10	72	0.9	43152	21	CELF59B1		Caenorhabditis elegans	7.36e-33
11	72	0.9	48088	22	CELY44E3A		Caenorhabditis elegans	7.36e-33
12	72	0.9	178553	19	AC006891		Caenorhabditis elegans	7.36e-33
13	72	0.9	245805	20	AC006752		Caenorhabditis elegans	7.36e-33

0.9	245805	20	AC006752	Caenorhabditis elegans	7.36e-33
0.9	298195	19	AC006890	Caenorhabditis elegans	7.36e-33
0.9	306131	19	AC006874	Caenorhabditis elegans	4.31e-32
0.9	319857	19	AC006782	Caenorhabditis elegans	7.36e-33
0.8	22886	22	CELC13F10	Caenorhabditis elegans	8.80e-24
0.8	37681	21	CEK05C4	Caenorhabditis elegans	8.97e-27
0.8	39184	19	CEY13F11	Caenorhabditis elegans	8.97e-27
0.8	40103	21	CELF20D6	Caenorhabditis elegans	2.66e-22
0.8	41564	21	CELF22F7	Caenorhabditis elegans	2.66e-22
0.8	42912	21	CELM03A1	Caenorhabditis elegans	2.66e-22
0.8	125590	21	CEY49E10	Caenorhabditis elegans	1.59e-24
0.8	183422	19	AC006905	Caenorhabditis elegans	2.66e-22
0.8	275138	19	CEY54E5	Caenorhabditis elegans	8.97e-27
0.8	298406	21	CEY75B8A	Caenorhabditis elegans	2.66e-22
0.8	317781	20	AC006906	Caenorhabditis elegans	4.86e-23
0.8	336638	19	CEY75B8	Caenorhabditis elegans	2.66e-22
0.7	11684	21	CELY22D07	Caenorhabditis elegans	1.20e-18
0.7	11775	22	CELT16H5	Caenorhabditis elegans	6.31e-18
0.7	12712	21	CEW09E7	Caenorhabditis elegans	2.26e-19
0.7	13610	21	CEK08F9	Caenorhabditis elegans	6.31e-18
0.7	19383	21	CER11H6	Caenorhabditis elegans	3.30e-17
0.7	21095	21	CELD1065	Caenorhabditis elegans	6.31e-18
0.7	23793	21	CELV09C3	Caenorhabditis elegans	7.86e-21
0.7	24709	21	CEC26H9A	Caenorhabditis elegans	1.20e-18
0.7	26894	22	CELY43I07	Caenorhabditis elegans	1.20e-18
0.7	30911	21	CER06C7	Caenorhabditis elegans	1.45e-21
0.7	32788	21	CEY33H1	Caenorhabditis elegans	6.31e-18
0.7	33883	21	CELV03E5	Caenorhabditis elegans	6.31e-18
0.7	34256	21	CELV10C8	Caenorhabditis elegans	6.31e-18
0.7	34852	22	CELV05F2	Caenorhabditis elegans	2.26e-19
0.7	35654	21	CER05D7	Caenorhabditis elegans	1.20e-18
0.7	35782	21	CELY49D11	Caenorhabditis elegans	1.20e-18
0.7	36004	21	CELV08A12	Caenorhabditis elegans	1.71e-16
0.7	36309	21	CEY45G2	Caenorhabditis elegans	1.71e-16
0.7	36404	22	CELD1037	Caenorhabditis elegans	6.31e-18
0.7	36454	19	AC006670	Caenorhabditis elegans	7.86e-21
0.7	36454	19	AC006670	Caenorhabditis elegans	1.20e-18
0.7	37628	21	CEY31D4	Caenorhabditis elegans	4.23e-20
0.7	37711	21	CEZK896	Caenorhabditis elegans	1.45e-21
0.7	38112	22	CELR08C7	Caenorhabditis elegans	2.26e-19
0.7	38419	22	CELY23C8	Caenorhabditis elegans	1.71e-16
0.7	38523	21	CEY39A1B	Caenorhabditis elegans	7.86e-21
0.7	38643	21	CELT03F1	Caenorhabditis elegans	2.26e-19
0.7	39565	21	CEK08E3	Caenorhabditis elegans	2.26e-19
0.7	39643	21	CELY25G6	Caenorhabditis elegans	2.26e-19
0.7	41553	21	CELY53G12	Caenorhabditis elegans	3.30e-17
0.7	42426	22	CELY39F7	Caenorhabditis elegans	1.71e-16
0.7	48096	21	CET20G5	Caenorhabditis elegans	7.86e-21
0.7	110000	19	CEY38E10	Caenorhabditis elegans	1.20e-18
0.7	115355	19	CEY55D9	Caenorhabditis elegans	1.20e-18
0.7	129060	21	CEY41C4A	Caenorhabditis elegans	3.30e-17
0.7	130294	19	CEY43F11	Caenorhabditis elegans	3.30e-17
0.7	150963	19	AC006727	Caenorhabditis elegans	1.20e-18
0.7	150963	19	AC006727	Caenorhabditis elegans	7.86e-21
0.7	152184	19	CEY70G10	Caenorhabditis elegans	7.86e-21
0.7	152878	21	CEY18D10A	Caenorhabditis elegans	4.23e-20
0.7	169226	19	AC006913	Caenorhabditis elegans	1.45e-21
0.7	171817	19	CEY55D11	Caenorhabditis elegans	1.20e-18
0.7	188972	20	AC006907	Caenorhabditis elegans	3.30e-17
0.7	200509	20	AC006910	Caenorhabditis elegans	1.71e-16
0.7	207370	19	AC006798	Caenorhabditis elegans	2.26e-19
0.7	232854	19	CEY40H4	Caenorhabditis elegans	3.30e-17
0.7	243820	19	CEY75B12	Caenorhabditis elegans	6.31e-18
0.7	247332	19	CEY18D10	Caenorhabditis elegans	4.23e-20
0.7	249640	19	CEY79H2	Caenorhabditis elegans	3.30e-17
0.7	254877	20	AC006904	Caenorhabditis elegans	3.30e-17
0.7	261002	19	CEY41C4	Caenorhabditis elegans	3.30e-17
0.7	262336	19	AC006786	Caenorhabditis elegans	6.31e-18
0.7	262336	19	AC006786	Caenorhabditis elegans	2.26e-19
0.7	263203	19	AC006709	Caenorhabditis elegans	7.86e-21
0.7	267118	20	AC006889	Caenorhabditis elegans	6.31e-18
0.7	269082	19	CEY76A2	Caenorhabditis elegans	1.71e-16
0.7	270192	19	CEY48C3	Caenorhabditis elegans	2.26e-19

87	C	53	0.7	274626	19	AC006903	Caenorhabditis elegans	1.20e-18	C	160	47	0.6	254877	20	AC006904	Caenorhabditis elegans	2.26e-14
88	C	56	0.7	274626	19	AC006903	Caenorhabditis elegans	7.86e-21	C	161	49	0.6	276829	20	AC006741	Caenorhabditis elegans	8.78e-16
89	C	53	0.7	276829	20	AC006741	Caenorhabditis elegans	1.20e-18	C	162	47	0.6	292390	19	AC006900	Caenorhabditis elegans	2.26e-14
90	C	56	0.7	286715	19	CEY45F3	Caenorhabditis elegans	7.86e-21	C	163	44	0.6	294136	20	AC006901	Caenorhabditis elegans	2.75e-12
91	C	51	0.7	292390	19	AC006900	Caenorhabditis elegans	3.30e-17	C	164	47	0.6	296699	19	CEY48A6	Caenorhabditis elegans	2.26e-14
92	C	53	0.7	297070	19	CEY47H10	Caenorhabditis elegans	1.20e-18	C	165	43	0.6	299202	19	AC006792	Caenorhabditis elegans	1.33e-11
93	C	52	0.7	297866	19	AC006794	Caenorhabditis elegans	6.31e-18	C	166	48	0.6	299719	19	AC006780	Caenorhabditis elegans	4.48e-15
94	C	50	0.7	298195	19	AC006890	Caenorhabditis elegans	1.71e-16	C	167	48	0.6	299719	19	AC006858	Caenorhabditis elegans	4.48e-15
95	C	55	0.7	298960	20	AC006896	Caenorhabditis elegans	7.86e-21	C	168	48	0.6	299919	19	AC006712	Caenorhabditis elegans	4.48e-15
96	C	56	0.7	299300	20	AC006881	Caenorhabditis elegans	7.86e-21	C	169	47	0.6	312267	19	AC006785	Caenorhabditis elegans	2.26e-14
97	C	56	0.7	299919	19	AC006712	Caenorhabditis elegans	7.86e-21	C	170	47	0.6	337565	19	CEY47D3	Caenorhabditis elegans	2.26e-14
98	C	53	0.7	306131	19	AC006874	Caenorhabditis elegans	1.20e-18	C	171	37	0.5	2144	21	CEVC50H2R	Caenorhabditis elegans	1.35e-07
99	C	51	0.7	312267	19	AC006785	Caenorhabditis elegans	3.30e-17	C	172	40	0.5	6751	21	CELMYOD	Caenorhabditis elegans	1.42e-09
100	C	53	0.7	315330	19	CEY46G5	Caenorhabditis elegans	1.20e-18	C	173	39	0.5	7035	21	CELCYT1A	Caenorhabditis elegans	6.56e-09
101	C	50	0.7	317781	20	AC006906	Caenorhabditis elegans	1.71e-16	C	174	35	0.5	7878	19	AC006831	Caenorhabditis elegans	2.60e-06
102	C	53	0.7	319857	19	AC006782	Caenorhabditis elegans	1.20e-18	C	175	37	0.5	9662	19	AC006775	Caenorhabditis elegans	1.35e-07
103	C	55	0.7	326074	19	CEY44A6	Caenorhabditis elegans	4.23e-20	C	176	36	0.5	10169	22	CELF36N01	Caenorhabditis elegans	5.96e-07
104	C	55	0.7	340801	19	AC006751	Caenorhabditis elegans	3.30e-17	C	177	39	0.5	10556	22	CELF53E2	Caenorhabditis elegans	6.56e-09
105	C	51	0.7	340801	19	AC006751	Caenorhabditis elegans	3.30e-17	C	178	35	0.5	12614	22	CELY76B12A	Caenorhabditis elegans	2.60e-06
106	C	43	0.6	4906	21	CELUNC60X	Caenorhabditis elegans	1.33e-11	C	179	38	0.5	12614	22	CELY76B12A	Caenorhabditis elegans	2.99e-08
107	C	47	0.6	8460	21	CEY52D3	Caenorhabditis elegans	2.26e-14	C	180	40	0.5	12734	21	CEH16D19	Caenorhabditis elegans	1.42e-09
108	C	47	0.6	8460	21	CEY52D3	Caenorhabditis elegans	2.26e-14	C	181	39	0.5	12734	21	CEH16D19	Caenorhabditis elegans	5.56e-09
109	C	43	0.6	10556	22	CELF53E2	Caenorhabditis elegans	1.33e-11	C	182	36	0.5	16820	21	CELK10E9	Caenorhabditis elegans	5.96e-07
110	C	47	0.6	18146	21	CEY39A1C	Caenorhabditis elegans	2.26e-14	C	183	35	0.5	16820	21	CELK10E9	Caenorhabditis elegans	2.60e-06
111	C	47	0.6	18655	22	CELY49G5B	Caenorhabditis elegans	2.26e-14	C	184	39	0.5	16938	22	CELT25D3	Caenorhabditis elegans	6.56e-09
112	C	45	0.6	20303	21	CEY81G3A	Caenorhabditis elegans	5.60e-13	C	185	38	0.5	17849	21	CELR09E12	Caenorhabditis elegans	2.99e-08
113	C	48	0.6	20960	21	CELF17A9	Caenorhabditis elegans	4.48e-15	C	186	37	0.5	18125	22	CELD2063	Caenorhabditis elegans	1.35e-07
114	C	48	0.6	23483	19	AC006627	Caenorhabditis elegans	4.48e-15	C	187	37	0.5	18655	22	CELY49G5B	Caenorhabditis elegans	1.35e-07
115	C	47	0.6	23928	21	CEY43F4A	Caenorhabditis elegans	2.26e-14	C	188	37	0.5	19371	21	CEK10G9	Caenorhabditis elegans	1.35e-07
116	C	49	0.6	26122	21	CELW02F12	Caenorhabditis elegans	8.78e-16	C	189	37	0.5	19529	19	AC006636	Caenorhabditis elegans	1.35e-07
117	C	43	0.6	29096	19	CEY09D11	Caenorhabditis elegans	1.33e-11	C	190	38	0.5	19588	21	CEFL8A11	Caenorhabditis elegans	2.99e-08
118	C	47	0.6	30225	21	CEY29C12	Caenorhabditis elegans	2.26e-14	C	191	41	0.5	19588	21	CEFL8A11	Caenorhabditis elegans	3.03e-10
119	C	47	0.6	32096	21	CEY21A3	Caenorhabditis elegans	2.26e-14	C	192	36	0.5	19934	21	CET23G7	Caenorhabditis elegans	5.96e-07
120	C	47	0.6	32205	21	CEK11D9	Caenorhabditis elegans	2.26e-14	C	193	41	0.5	20019	21	CER17	Caenorhabditis elegans	3.03e-10
121	C	49	0.6	32218	21	CELR02D3	Caenorhabditis elegans	8.78e-16	C	194	36	0.5	20836	22	CEFL3F11	Caenorhabditis elegans	5.96e-07
122	C	47	0.6	33238	21	CET06E6	Caenorhabditis elegans	2.26e-14	C	195	42	0.5	22886	22	CELC13F10	Caenorhabditis elegans	6.39e-11
123	C	47	0.6	33539	22	CELF54E7	Caenorhabditis elegans	2.26e-14	C	196	35	0.5	23483	19	AC006627	Caenorhabditis elegans	2.60e-06
124	C	49	0.6	33883	21	CELK03E5	Caenorhabditis elegans	8.78e-16	C	197	36	0.5	23793	21	CELW09C3	Caenorhabditis elegans	5.96e-07
125	C	45	0.6	33963	21	CELT22F3	Caenorhabditis elegans	5.60e-13	C	198	35	0.5	24709	21	CEC26H9A	Caenorhabditis elegans	2.60e-06
126	C	44	0.6	34132	21	CELT26C12	Caenorhabditis elegans	2.26e-14	C	199	35	0.5	25371	22	CELY23H5A	Caenorhabditis elegans	2.60e-06
127	C	47	0.6	34728	21	CELF41H10	Caenorhabditis elegans	2.26e-14	C	200	35	0.5	25371	19	AC006728	Caenorhabditis elegans	2.60e-06
128	C	45	0.6	34907	21	CELM01B12	Caenorhabditis elegans	5.60e-13	C	201	35	0.5	26894	22	CELH43I07	Caenorhabditis elegans	2.60e-06
129	C	48	0.6	35169	21	CELC44E4	Caenorhabditis elegans	4.48e-15	C	202	37	0.5	27396	21	CELC54G6	Caenorhabditis elegans	1.35e-07
130	C	43	0.6	35776	21	CELW02G9	Caenorhabditis elegans	1.33e-11	C	203	35	0.5	27567	21	CELT27C4	Caenorhabditis elegans	2.60e-06
131	C	43	0.6	35855	21	CELC38C3	Caenorhabditis elegans	1.33e-11	C	204	41	0.5	27748	22	CELH34C03	Caenorhabditis elegans	3.03e-10
132	C	47	0.6	35989	21	CEZK1320	Caenorhabditis elegans	2.26e-14	C	205	37	0.5	27777	21	CEY43D2	Caenorhabditis elegans	1.35e-07
133	C	43	0.6	36306	21	CEM142	Caenorhabditis elegans	1.33e-11	C	206	37	0.5	27809	21	CEY38H4	Caenorhabditis elegans	1.35e-07
134	C	45	0.6	36999	21	CELM01B11	Caenorhabditis elegans	5.60e-13	C	207	35	0.5	27809	21	CEY38H4	Caenorhabditis elegans	2.60e-06
135	C	48	0.6	38643	21	CELT03F1	Caenorhabditis elegans	4.48e-15	C	208	37	0.5	27832	21	CEZK1128	Caenorhabditis elegans	1.35e-07
136	C	45	0.6	39086	21	CEK07A1	Caenorhabditis elegans	5.60e-13	C	209	35	0.5	28026	22	CELY66H1A	Caenorhabditis elegans	2.60e-06
137	C	44	0.6	39273	22	CELK08D9	Caenorhabditis elegans	2.75e-12	C	210	38	0.5	28762	21	CEZC376	Caenorhabditis elegans	2.99e-08
138	C	44	0.6	39565	21	CEK08E3	Caenorhabditis elegans	2.75e-12	C	211	38	0.5	29096	19	CEY09D11	Caenorhabditis elegans	2.99e-08
139	C	46	0.6	39784	21	CEC14A4	Caenorhabditis elegans	1.13e-13	C	212	37	0.5	29214	21	CELC50F2	Caenorhabditis elegans	1.35e-07
140	C	44	0.6	40437	21	CELT10B5	Caenorhabditis elegans	2.75e-12	C	213	40	0.5	29214	21	CELC50F2	Caenorhabditis elegans	1.42e-09
141	C	47	0.6	41553	21	CELF53G12	Caenorhabditis elegans	2.26e-14	C	214	40	0.5	29363	21	CEY37D6	Caenorhabditis elegans	1.42e-09
142	C	48	0.6	41645	21	CELC03H5	Caenorhabditis elegans	4.48e-15	C	215	42	0.5	29786	21	CEC55A6	Caenorhabditis elegans	6.39e-11
143	C	43	0.6	43410	21	CEC01G6	Caenorhabditis elegans	1.33e-11	C	216	37	0.5	30274	21	CEY45H11	Caenorhabditis elegans	1.35e-07
144	C	45	0.6	44132	22	CELF52C12	Caenorhabditis elegans	5.60e-13	C	217	40	0.5	31244	21	CEY43F4B	Caenorhabditis elegans	1.42e-09
145	C	48	0.6	78153	21	CEY53C10A	Caenorhabditis elegans	4.48e-15	C	218	38	0.5	31255	21	CER01H10	Caenorhabditis elegans	2.99e-08
146	C	44	0.6	110000	19	CEY57A10	Caenorhabditis elegans	2.75e-12	C	219	40	0.5	31950	21	CEC38H2	Caenorhabditis elegans	1.42e-09
147	C	48	0.6	110000	19	CEY57A10	Caenorhabditis elegans	4.48e-15	C	220	36	0.5	31950	21	CEC38H2	Caenorhabditis elegans	5.96e-07
148	C	47	0.6	110000	19	CEY81G3	Caenorhabditis elegans	2.26e-14	C	221	37	0.5	32048	21	CELF57C9	Caenorhabditis elegans	1.35e-07
149	C	45	0.6	112726	19	CEY21F11	Caenorhabditis elegans	5.60e-13	C	222	38	0.5	32205	21	CEK11D9	Caenorhabditis elegans	2.99e-08
150	C	44	0.6	140702	20	AC006888	Caenorhabditis elegans	2.75e-12	C	223	39	0.5	32215	21	CEW02B9	Caenorhabditis elegans	6.56e-09
151	C	48	0.6	145920	19	AC006710	Caenorhabditis elegans	4.48e-15	C	224	42	0.5	32218	21	CELR02D3	Caenorhabditis elegans	6.39e-11
152	C	44	0.6	159453	19	AC006732	Caenorhabditis elegans	2.75e-12	C	225	36	0.5	32556	22	CELT27C10	Caenorhabditis elegans	5.96e-07
153	C	46	0.6	163125	19	AC006324	Homo sapiens clone DJ1	1.13e-13	C	226	41	0.5	32677	21	CEC08F8	Caenorhabditis elegans	3.03e-10
154	C	44	0.6	173140	19	AC004867	Homo sapiens clone DJ0	2.75e-12	C	227	35	0.5	32715	21	CEY54F12	Caenorhabditis elegans	2.60e-06
155	C	43	0.6	201746	20	AC006895	Caenorhabditis elegans	1.33e-11	C	228	40	0.5	32715	21	CEY54F12	Caenorhabditis elegans	1.42e-09
156	C	48	0.6	201746	20	AC006895	Caenorhabditis elegans	4.48e-15	C	229	35	0.5	32919	19	CEH37L19	Caenorhabditis elegans	2.60e-06
157	C	49	0.6	206217	19	AC006754	Caenorhabditis elegans	8.78e-16	C	230	39	0.5	33000	21	CEK11H3	Caenorhabditis elegans	6.56e-09
158	C	46	0.6	207370	19	AC006798	Caenorhabditis elegans	1.13e-13	C	231	37	0.5	33156	21	CET25E12	Caenorhabditis elegans	1.35e-07
159	C	47	0.6	242893	19	CEY53C12	Caenorhabditis elegans	2.26e-14	C	232	39	0.5	33238	21	CET06E6	Caenorhabditis elegans	6.56e-09

C	233	39	0.5	33270	21	CELR02F11	Caenorhabditis elegans	6.56e-09	C	306	35	0.5	42537	19	AC006645	Caenorhabditis elegans	2.60e-06
C	234	36	0.5	33477	21	CET07C4	Caenorhabditis elegans	5.96e-07	C	307	42	0.5	42703	21	CEC09F9	Caenorhabditis elegans	6.39e-11
C	235	39	0.5	33477	21	CET07C4	Caenorhabditis elegans	6.56e-09	C	308	35	0.5	42923	21	CELC24H12	Caenorhabditis elegans	2.60e-06
C	236	40	0.5	33511	21	CEZK1010	Caenorhabditis elegans	1.42e-09	C	309	35	0.5	42995	21	CELF31F4	Caenorhabditis elegans	2.60e-06
C	237	36	0.5	33520	21	CET02E1	Caenorhabditis elegans	5.96e-07	C	310	36	0.5	43148	21	CEFS2F12	Caenorhabditis elegans	1.35e-07
C	238	37	0.5	33650	21	CEK01A11	Caenorhabditis elegans	1.35e-07	C	311	37	0.5	43395	21	CEY66A7A	Caenorhabditis elegans	5.96e-07
C	239	38	0.5	33921	21	CEW09D10	Caenorhabditis elegans	2.99e-08	C	312	36	0.5	43395	21	CEY66A7A	Caenorhabditis elegans	5.96e-07
C	240	36	0.5	34256	21	CEW09D10	Caenorhabditis elegans	5.96e-07	C	313	37	0.5	43726	21	CELC32E8	Caenorhabditis elegans	1.35e-07
C	241	35	0.5	34350	21	CELF56H1	Caenorhabditis elegans	2.60e-06	C	314	36	0.5	45348	19	AC006624	Caenorhabditis elegans	5.96e-07
C	242	38	0.5	34576	21	CET23D8	Caenorhabditis elegans	2.99e-08	C	315	39	0.5	48088	22	CEY44E3A	Caenorhabditis elegans	6.56e-09
C	243	41	0.5	34775	22	CEW08F4	Caenorhabditis elegans	3.03e-10	C	316	40	0.5	48173	19	CEY38H8	Caenorhabditis elegans	1.42e-09
C	244	36	0.5	34831	21	CEC47G2	Caenorhabditis elegans	5.96e-07	C	317	40	0.5	48985	19	CEW03G8	Caenorhabditis elegans	1.42e-09
C	245	36	0.5	35077	21	CEY38H8A	Caenorhabditis elegans	5.96e-07	C	318	41	0.5	48985	19	CEW03G8	Caenorhabditis elegans	3.03e-10
C	246	40	0.5	35077	21	CEY38H8A	Caenorhabditis elegans	1.42e-09	C	319	39	0.5	67943	19	AC006722	Caenorhabditis elegans	6.56e-09
C	247	38	0.5	35165	21	CELC56C10	Caenorhabditis elegans	2.99e-08	C	320	41	0.5	67943	19	AC006722	Caenorhabditis elegans	3.03e-10
C	248	35	0.5	35503	21	CEW09D6	Caenorhabditis elegans	2.60e-06	C	321	37	0.5	75073	21	CEY48A6B	Caenorhabditis elegans	1.35e-07
C	249	38	0.5	35564	21	CELT22B11	Caenorhabditis elegans	2.99e-08	C	322	37	0.5	95182	21	CEY54G11A	Caenorhabditis elegans	1.35e-07
C	250	36	0.5	35654	21	CER05D7	Caenorhabditis elegans	5.96e-07	C	323	37	0.5	95182	21	CEY54G11A	Caenorhabditis elegans	1.35e-07
C	251	36	0.5	35804	21	CEF10C2	Caenorhabditis elegans	5.96e-07	C	324	39	0.5	95968	21	CEY47D3B	Caenorhabditis elegans	6.56e-09
C	252	42	0.5	35879	21	CEW02A2	Caenorhabditis elegans	6.39e-11	C	325	41	0.5	101584	19	AC006793	Caenorhabditis elegans	3.03e-10
C	253	35	0.5	36004	21	CEW08A12	Caenorhabditis elegans	2.60e-06	C	326	38	0.5	101584	19	AC006793	Caenorhabditis elegans	2.99e-08
C	254	36	0.5	36302	21	CEZC482	Caenorhabditis elegans	5.96e-07	C	327	40	0.5	110000	19	CEY39E4	Caenorhabditis elegans	1.42e-09
C	255	40	0.5	36306	21	CEM142	Caenorhabditis elegans	1.42e-09	C	328	40	0.5	110000	19	CEY39E4	Caenorhabditis elegans	1.42e-09
C	256	35	0.5	36654	21	CEY45F3A	Caenorhabditis elegans	2.60e-06	C	329	39	0.5	110000	19	CEY54E2	Caenorhabditis elegans	6.56e-09
C	257	39	0.5	36780	19	CEH10N23	Caenorhabditis elegans	6.56e-09	C	330	38	0.5	110000	19	CEY53H1	Caenorhabditis elegans	2.99e-08
C	258	37	0.5	37342	21	CELC18G1	Caenorhabditis elegans	1.35e-07	C	331	38	0.5	110000	19	CEY81G3	Caenorhabditis elegans	2.99e-08
C	259	36	0.5	37353	21	CET12D8	Caenorhabditis elegans	5.96e-07	C	332	36	0.5	110000	19	CEY39A1	Caenorhabditis elegans	5.96e-07
C	260	37	0.5	37545	21	CET21C9	Caenorhabditis elegans	1.35e-07	C	333	36	0.5	110000	19	CEY11B2	Caenorhabditis elegans	5.96e-07
C	261	42	0.5	37681	21	CEK05C4	Caenorhabditis elegans	6.39e-11	C	334	41	0.5	110000	19	CEY54E2	Caenorhabditis elegans	3.03e-10
C	262	36	0.5	37711	21	CEZK896	Caenorhabditis elegans	5.96e-07	C	335	40	0.5	110000	19	CEY39A1	Caenorhabditis elegans	1.42e-09
C	263	36	0.5	37738	21	CELF32B5	Caenorhabditis elegans	5.96e-07	C	336	39	0.5	110960	21	CEY39A1A	Caenorhabditis elegans	6.56e-09
C	264	36	0.5	37805	22	CEW03G1	Caenorhabditis elegans	5.96e-07	C	337	40	0.5	110960	21	CEY39A1A	Caenorhabditis elegans	1.42e-09
C	265	35	0.5	37805	22	CEW03G1	Caenorhabditis elegans	2.60e-06	C	338	35	0.5	115355	19	CEY55D9	Caenorhabditis elegans	2.60e-06
C	266	40	0.5	37881	21	CELK09H9	Caenorhabditis elegans	1.35e-07	C	339	42	0.5	125590	21	CEY49E10	Caenorhabditis elegans	6.39e-11
C	267	37	0.5	38112	22	CELR08C7	Caenorhabditis elegans	1.35e-07	C	340	41	0.5	132742	21	CEY37D8A	Caenorhabditis elegans	3.03e-10
C	268	40	0.5	38152	21	CEW03B1	Caenorhabditis elegans	1.42e-09	C	341	42	0.5	132742	21	CEY37D8A	Caenorhabditis elegans	3.03e-10
C	269	40	0.5	38152	21	CEW03B1	Caenorhabditis elegans	1.42e-09	C	342	41	0.5	135550	19	AC006721	Caenorhabditis elegans	2.99e-08
C	270	35	0.5	38561	19	AC006604	Caenorhabditis elegans	2.60e-06	C	343	38	0.5	135550	19	AC006721	Caenorhabditis elegans	1.35e-07
C	271	38	0.5	38561	19	AC006604	Caenorhabditis elegans	2.99e-08	C	344	37	0.5	136764	19	CEY24E3	Caenorhabditis elegans	6.56e-09
C	272	37	0.5	38570	21	CELC06A8	Caenorhabditis elegans	1.35e-07	C	345	39	0.5	140702	20	AC006888	Caenorhabditis elegans	1.42e-09
C	273	39	0.5	38801	19	AC006692	Caenorhabditis elegans	6.56e-09	C	346	40	0.5	150641	21	CEY41E3	Caenorhabditis elegans	2.99e-08
C	274	41	0.5	38846	19	AC006696	Caenorhabditis elegans	3.03e-10	C	347	38	0.5	151727	20	AC006894	Caenorhabditis elegans	1.35e-07
C	275	39	0.5	38876	22	CELR119	Caenorhabditis elegans	6.56e-09	C	348	37	0.5	152878	21	CEY18D10A	Caenorhabditis elegans	6.39e-11
C	276	41	0.5	38890	21	CELC14C11	Caenorhabditis elegans	3.03e-10	C	349	42	0.5	159453	19	AC006732	Caenorhabditis elegans	1.35e-07
C	277	40	0.5	38890	21	CELC14C11	Caenorhabditis elegans	1.42e-09	C	350	37	0.5	166214	20	AC006735	Caenorhabditis elegans	2.99e-08
C	278	42	0.5	38980	21	CER06C1	Caenorhabditis elegans	6.39e-11	C	351	38	0.5	178443	19	CEY38F1	Caenorhabditis elegans	3.03e-10
C	279	42	0.5	38984	22	CELF56E10	Caenorhabditis elegans	6.39e-11	C	352	41	0.5	178443	19	CEY38F1	Caenorhabditis elegans	3.03e-10
C	280	40	0.5	39184	19	CEF12F11	Caenorhabditis elegans	1.42e-09	C	353	41	0.5	178553	19	AC006891	Caenorhabditis elegans	1.42e-09
C	281	42	0.5	39211	21	CEC36F7	Caenorhabditis elegans	6.39e-11	C	354	40	0.5	179854	19	CEY19D2	Caenorhabditis elegans	6.39e-11
C	282	36	0.5	39235	21	CELF32D1	Caenorhabditis elegans	5.96e-07	C	355	42	0.5	179854	19	CEY19D2	Caenorhabditis elegans	6.56e-09
C	283	40	0.5	39333	21	CEB0564	Caenorhabditis elegans	1.42e-09	C	356	39	0.5	186550	19	CEY44F5	Caenorhabditis elegans	2.60e-06
C	284	35	0.5	39614	22	CELB0336	Caenorhabditis elegans	2.60e-06	C	357	35	0.5	191857	19	CEY32B12	Caenorhabditis elegans	1.42e-09
C	285	38	0.5	39931	21	CELC54E4	Caenorhabditis elegans	2.99e-08	C	358	40	0.5	193188	20	AC006884	Caenorhabditis elegans	6.56e-09
C	286	40	0.5	39941	21	CELF39G3	Caenorhabditis elegans	1.42e-09	C	359	39	0.5	197735	19	CEY66A7	Caenorhabditis elegans	5.96e-07
C	287	37	0.5	39941	21	CELF39G3	Caenorhabditis elegans	1.35e-07	C	360	37	0.5	200509	20	AC006910	Caenorhabditis elegans	1.35e-07
C	288	40	0.5	39973	21	CEM106	Caenorhabditis elegans	6.39e-11	C	361	37	0.5	204594	19	AC006788	Caenorhabditis elegans	2.99e-08
C	289	42	0.5	39973	21	CEM106	Caenorhabditis elegans	6.39e-11	C	362	38	0.5	224525	19	CEY70C5	Caenorhabditis elegans	5.96e-07
C	290	42	0.5	40437	21	CELT10B5	Caenorhabditis elegans	6.39e-11	C	363	37	0.5	224525	19	CEY70C5	Caenorhabditis elegans	5.96e-07
C	291	41	0.5	40453	21	CEC09H10	Caenorhabditis elegans	3.03e-10	C	364	36	0.5	224746	19	CEY56A3	Caenorhabditis elegans	1.35e-07
C	292	35	0.5	40662	21	CEY32B12B	Caenorhabditis elegans	2.60e-06	C	365	37	0.5	232854	19	CEY40H4	Caenorhabditis elegans	6.56e-09
C	293	39	0.5	40780	21	CEM03C11	Caenorhabditis elegans	6.56e-09	C	366	39	0.5	233941	19	CEY52B11	Caenorhabditis elegans	1.35e-07
C	294	36	0.5	40921	21	CELB0432	Caenorhabditis elegans	5.96e-07	C	367	37	0.5	247332	19	CEY18D10	Caenorhabditis elegans	6.56e-09
C	295	35	0.5	40999	21	CELF56A6	Caenorhabditis elegans	2.60e-06	C	368	42	0.5	256941	19	CEY62E10	Caenorhabditis elegans	1.42e-09
C	296	41	0.5	40999	21	CELF56A6	Caenorhabditis elegans	3.03e-10	C	369	40	0.5	256941	19	CEY62E10	Caenorhabditis elegans	1.35e-07
C	297	37	0.5	41179	21	CELM01D7	Caenorhabditis elegans	1.35e-07	C	370	37	0.5	257728	19	AC006846	Caenorhabditis elegans	1.42e-09
C	298	39	0.5	41258	21	CELC08F1	Caenorhabditis elegans	6.56e-09	C	371	40	0.5	260699	20	AC006893	Caenorhabditis elegans	5.96e-07
C	299	39	0.5	41313	21	CEC16C10	Caenorhabditis elegans	6.56e-09	C	372	36	0.5	263203	19	AC006709	Caenorhabditis elegans	2.99e-08
C	300	39	0.5	41316	22	CELC01B4	Caenorhabditis elegans	6.56e-09	C	373	38	0.5	267118	20	AC006889	Caenorhabditis elegans	2.99e-08
C	301	41	0.5	41316	22	CELC01B4	Caenorhabditis elegans	3.03e-10	C	374	38	0.5	270192	19	CEY48C3	Caenorhabditis elegans	6.56e-09
C	302	35	0.5	41645	21	CELC03H5	Caenorhabditis elegans	2.60e-06	C	375	39	0.5	274498	19	AC006765	Caenorhabditis elegans	6.39e-11
C	303	41	0.5	41778	21	CELM04G7	Caenorhabditis elegans	3.03e-10	C	376	42	0.5	275138	19	CEY54E5	Caenorhabditis elegans	3.03e-10
C	304	40	0.5	42282	21	CELB0304	Caenorhabditis elegans	1.42e-09	C	377	41	0.5	278007	19	AC006799	Caenorhabditis elegans	6.56e-09
C	305	42	0.5	42391	21	CEF28F8	Caenorhabditis elegans	6.39e-11	C	378	39	0.5	286715	19	CEY45F3	Caenorhabditis elegans	6.56e-09

C 379	36	0.5	291622	19	AC006796	Caenorhabditis elegans	5.96e-07	452	34	0.4	23113	21	CEL26A8	Caenorhabditis elegans	1.11e-05
C 380	36	0.5	291821	19	CEY48E1	Caenorhabditis elegans	5.96e-07	453	32	0.4	23114	21	CEL54D11	Caenorhabditis elegans	1.94e-04
C 381	37	0.5	296699	19	CEY48A6	Caenorhabditis elegans	1.35e-07	454	33	0.4	23114	21	CEL54D11	Caenorhabditis elegans	4.70e-05
C 382	36	0.5	297070	19	CEY47H10	Caenorhabditis elegans	5.96e-07	455	33	0.4	23536	21	CEL28H1	Caenorhabditis elegans	4.70e-05
C 383	40	0.5	297866	19	AC006794	Caenorhabditis elegans	1.42e-09	456	29	0.4	23928	21	CEY43F4A	Caenorhabditis elegans	1.21e-02
C 384	39	0.5	298950	20	AC006896	Caenorhabditis elegans	6.56e-09	457	33	0.4	24281	21	CEC06H2	Caenorhabditis elegans	4.70e-05
C 385	38	0.5	299202	19	AC006792	Caenorhabditis elegans	2.99e-08	458	30	0.4	25360	21	CER90	Caenorhabditis elegans	4.70e-03
C 386	35	0.5	299308	19	AC006898	Caenorhabditis elegans	2.60e-06	459	28	0.4	25371	22	CELY23H5A	Caenorhabditis elegans	3.12e-03
C 387	41	0.5	299308	19	AC006898	Caenorhabditis elegans	3.03e-10	460	28	0.4	25371	19	AC006728	Caenorhabditis elegans	4.59e-02
C 388	35	0.5	299719	19	AC006858	Caenorhabditis elegans	2.60e-06	461	32	0.4	25468	21	CEFL47F	Caenorhabditis elegans	4.59e-02
C 389	35	0.5	299719	19	AC006780	Caenorhabditis elegans	2.60e-06	462	31	0.4	25600	21	CELT20F5	Caenorhabditis elegans	1.94e-04
C 390	42	0.5	299782	19	AC006844	Caenorhabditis elegans	6.39e-11	463	32	0.4	26209	21	CEY39E4A	Caenorhabditis elegans	7.87e-04
C 391	41	0.5	309026	19	AC006760	Caenorhabditis elegans	3.03e-10	464	33	0.4	26253	21	CEY70G10A	Caenorhabditis elegans	4.70e-05
C 392	38	0.5	309026	19	AC006760	Caenorhabditis elegans	6.39e-11	465	30	0.4	26343	21	CEY45F10A	Caenorhabditis elegans	3.12e-03
C 393	42	0.5	314495	19	CEY67H2	Caenorhabditis elegans	6.39e-11	466	37	0.4	26343	21	CEY45F10A	Caenorhabditis elegans	1.70e-01
C 394	42	0.5	315330	19	CEY46G5	Caenorhabditis elegans	6.39e-11	467	33	0.4	27111	21	CELC45E1	Caenorhabditis elegans	4.70e-05
C 395	37	0.5	335822	19	CEY54G11	Caenorhabditis elegans	1.35e-07	468	27	0.4	27178	21	CELF21F3	Caenorhabditis elegans	1.21e-02
C 396	37	0.5	335822	19	CEY54G11	Caenorhabditis elegans	1.35e-07	469	29	0.4	27236	21	CEY32F6A	Caenorhabditis elegans	1.21e-02
C 397	42	0.5	336638	19	CEY7588	Caenorhabditis elegans	6.39e-11	470	29	0.4	27777	21	CEY32F6A	Caenorhabditis elegans	1.21e-02
C 398	42	0.5	337565	19	CEY47D3	Caenorhabditis elegans	6.39e-11	471	29	0.4	27832	21	CEZK1128	Caenorhabditis elegans	1.21e-02
C 399	29	0.4	2229	21	CEPHA1	C.elegans pha-1 mRNA.	1.21e-02	472	29	0.4	28678	21	CELT04D1	Caenorhabditis elegans	1.21e-02
C 400	32	0.4	2229	21	CEPHA1	C.elegans pha-1 mRNA.	1.94e-04	473	29	0.4	28678	21	CELT04D1	Caenorhabditis elegans	1.21e-02
C 401	28	0.4	5290	20	AC006886	Caenorhabditis elegans	4.59e-02	474	28	0.4	28678	21	CELT04D1	Caenorhabditis elegans	1.21e-02
C 402	30	0.4	5535	21	AB000802	Caenorhabditis elegans	3.12e-03	475	28	0.4	28871	21	CEC47B2	Caenorhabditis elegans	4.59e-02
C 403	31	0.4	5535	21	AB000802	Caenorhabditis elegans	7.87e-04	476	31	0.4	29085	21	CEY59C6	Caenorhabditis elegans	4.59e-02
C 404	29	0.4	7092	21	CEPHALD	C.elegans pha-1 gene.	1.21e-02	477	32	0.4	29283	21	CEFL4B6	Caenorhabditis elegans	7.87e-04
C 405	32	0.4	7092	21	CEPHALD	C.elegans pha-1 gene.	1.94e-04	478	29	0.4	29303	21	CEY57G4	Caenorhabditis elegans	1.94e-04
C 406	29	0.4	7141	21	CELFEM1	C.elegans fem-1 gene.	1.21e-02	479	28	0.4	29364	21	CEC27B7	Caenorhabditis elegans	4.59e-02
C 407	31	0.4	7141	21	CELFEM1	C.elegans fem-1 gene.	7.87e-04	480	32	0.4	30098	21	CEK09E9	Caenorhabditis elegans	1.94e-04
C 408	33	0.4	7988	21	CEY52B11C	Caenorhabditis elegans	4.70e-05	481	31	0.4	30522	21	CELM01H9	Caenorhabditis elegans	7.87e-04
C 409	28	0.4	9274	21	CEZK256	Caenorhabditis elegans	4.59e-02	482	30	0.4	30827	21	CEW09H1	Caenorhabditis elegans	3.12e-03
C 410	31	0.4	9314	22	CELM06B4	Caenorhabditis elegans	7.87e-04	483	31	0.4	30827	21	CEW09H1	Caenorhabditis elegans	3.12e-03
C 411	31	0.4	9618	21	CELT13E5	Caenorhabditis elegans	7.87e-04	484	30	0.4	30911	21	CEW09H1	Caenorhabditis elegans	7.87e-04
C 412	30	0.4	11684	21	CELT22D07	Caenorhabditis elegans	3.12e-03	485	33	0.4	31264	21	CELF40E3	Caenorhabditis elegans	7.87e-04
C 413	28	0.4	12712	21	CEW09E7	Caenorhabditis elegans	4.59e-02	486	29	0.4	31273	21	CEW05E10	Caenorhabditis elegans	4.70e-05
C 414	27	0.4	12847	22	CELY14H12B	Caenorhabditis elegans	1.70e-01	487	34	0.4	32209	19	AC006663	Caenorhabditis elegans	1.21e-02
C 415	28	0.4	13120	21	CELC10B5	Caenorhabditis elegans	7.87e-04	488	32	0.4	32263	19	AC006776	Caenorhabditis elegans	1.11e-05
C 416	31	0.4	13610	21	CEK08F9	Caenorhabditis elegans	7.87e-04	489	34	0.4	32263	19	AC006776	Caenorhabditis elegans	1.94e-04
C 417	34	0.4	13877	21	CEY54E12	Caenorhabditis elegans	1.11e-05	490	30	0.4	32458	21	CEY49E11	Caenorhabditis elegans	3.12e-03
C 418	31	0.4	14473	21	CELF35D6	Caenorhabditis elegans	7.87e-04	491	31	0.4	32556	22	CELT27C10	Caenorhabditis elegans	7.87e-04
C 419	29	0.4	14473	21	CELF35D6	Caenorhabditis elegans	1.21e-02	492	28	0.4	32563	22	CELF54D10	Caenorhabditis elegans	4.59e-02
C 420	31	0.4	14759	21	CEK12D12	Caenorhabditis elegans	7.87e-04	493	34	0.4	32591	21	CEFL6D3	Caenorhabditis elegans	1.11e-05
C 421	33	0.4	14759	21	CEK12D12	Caenorhabditis elegans	4.70e-05	494	33	0.4	32612	21	CEFL6D3	Caenorhabditis elegans	4.70e-05
C 422	32	0.4	15704	21	CELF37F2	Caenorhabditis elegans	1.94e-04	495	31	0.4	32700	21	CEFL6D3	Caenorhabditis elegans	4.70e-05
C 423	28	0.4	16938	22	CELT25D3	Caenorhabditis elegans	4.59e-02	496	33	0.4	32700	21	CEFL6D3	Caenorhabditis elegans	7.87e-04
C 424	27	0.4	17691	21	CEY57A10	Caenorhabditis elegans	1.70e-01	497	27	0.4	32707	21	CELT12F5	Caenorhabditis elegans	1.21e-02
C 425	31	0.4	17716	21	CELM06E11	Caenorhabditis elegans	7.87e-04	498	29	0.4	32880	21	CEY40F12	Caenorhabditis elegans	4.59e-02
C 426	28	0.4	17716	21	CELM06E11	Caenorhabditis elegans	7.87e-04	499	28	0.4	32919	19	CEH37L19	Caenorhabditis elegans	1.70e-01
C 427	31	0.4	18227	19	AC006768	Caenorhabditis elegans	4.59e-02	500	27	0.4	32963	21	CEY33H2	Caenorhabditis elegans	1.70e-01
C 428	32	0.4	18227	19	AC006768	Caenorhabditis elegans	7.87e-04	501	27	0.4	32963	21	CEY33H2	Caenorhabditis elegans	4.59e-02
C 429	31	0.4	18351	21	CEY09E8	Caenorhabditis elegans	7.87e-04	502	28	0.4	32963	21	CEY33H2	Caenorhabditis elegans	1.11e-05
C 430	31	0.4	18351	21	CEY09E8	Caenorhabditis elegans	7.87e-04	503	34	0.4	33000	21	CEK11H3	Caenorhabditis elegans	1.94e-04
C 431	31	0.4	18617	21	CEM04D5	Caenorhabditis elegans	7.87e-04	504	32	0.4	33038	21	CELB0261	Caenorhabditis elegans	1.21e-02
C 432	31	0.4	18946	21	CEC27D8	Caenorhabditis elegans	7.87e-04	505	29	0.4	33164	21	CEY35C5	Caenorhabditis elegans	1.94e-04
C 433	32	0.4	19020	21	CELR13H8	Caenorhabditis elegans	7.87e-04	506	29	0.4	33200	21	CEY54B3	Caenorhabditis elegans	1.21e-02
C 434	29	0.4	19020	21	CELR13H8	Caenorhabditis elegans	1.21e-02	507	32	0.4	33274	21	CEY52B5	Caenorhabditis elegans	1.94e-04
C 435	33	0.4	19383	21	CEK11H6	Caenorhabditis elegans	1.21e-02	508	31	0.4	33490	21	CEZK20	Caenorhabditis elegans	7.87e-04
C 436	30	0.4	19442	21	CEK01G5	Caenorhabditis elegans	3.12e-03	509	32	0.4	33511	21	CEZK1010	Caenorhabditis elegans	7.87e-04
C 437	29	0.4	19442	21	CEK01G5	Caenorhabditis elegans	4.70e-05	510	32	0.4	33539	22	CELF54E7	Caenorhabditis elegans	1.94e-04
C 438	31	0.4	19529	19	AC006636	Caenorhabditis elegans	7.87e-04	511	30	0.4	33588	21	CELK10G6	Caenorhabditis elegans	3.12e-03
C 439	31	0.4	19532	21	CELC37F5	Caenorhabditis elegans	7.87e-04	512	28	0.4	33770	21	CEFL5A4	Caenorhabditis elegans	4.59e-02
C 440	28	0.4	19934	21	CET23G7	Caenorhabditis elegans	4.59e-02	513	30	0.4	33770	21	CEFL5A4	Caenorhabditis elegans	3.12e-03
C 441	32	0.4	20303	19	AC006749	Caenorhabditis elegans	1.94e-04	514	30	0.4	33921	21	CEW09D10	Caenorhabditis elegans	3.12e-03
C 442	31	0.4	20303	21	CEY81G3A	Caenorhabditis elegans	7.87e-04	515	33	0.4	33963	21	CELT22F3	Caenorhabditis elegans	3.12e-03
C 443	32	0.4	20303	19	AC006749	Caenorhabditis elegans	1.94e-04	516	31	0.4	34122	22	CELY66H1B	Caenorhabditis elegans	4.70e-05
C 444	32	0.4	20486	21	CELF23F1	Caenorhabditis elegans	1.94e-04	517	33	0.4	34132	21	CELT26C12	Caenorhabditis elegans	7.87e-04
C 445	32	0.4	20486	21	CELF23F1	Caenorhabditis elegans	1.94e-04	518	31	0.4	34268	21	CEW02D7	Caenorhabditis elegans	4.70e-05
C 446	27	0.4	20507	19	AC006820	Caenorhabditis elegans	1.94e-04	519	31	0.4	34305	21	CEW02B12	Caenorhabditis elegans	7.87e-04
C 447	28	0.4	21083	21	CEH04D03	Caenorhabditis elegans	4.59e-02	520	29	0.4	34348	21	CELK10C9	Caenorhabditis elegans	1.21e-02
C 448	31	0.4	21836	21	CELT2K40	Caenorhabditis elegans	7.87e-04	521	27	0.4	34348	21	CELK10C9	Caenorhabditis elegans	1.70e-01
C 449	27	0.4	21870	21	CET01H3	Caenorhabditis elegans	1.70e-01	522	31	0.4	34432	19	AC006693	Caenorhabditis elegans	7.87e-04
C 450	28	0.4	22729	21	CELF53F10	Caenorhabditis elegans	4.59e-02	523	27	0.4	34500	21	CET16H12	Caenorhabditis elegans	1.70e-01
C 451	32	0.4	22729	21	CELF53F10	Caenorhabditis elegans	1.94e-04	524	31	0.4	34500	21	CET16H12	Caenorhabditis elegans	7.87e-04

525	33	0.4	34511	21	CELZC404	Caenorhabditis elegans	4.70e-05	598	32	0.4	38990	21	CEF36D3	Caenorhabditis elegans	1.94e-04
526	33	0.4	34511	21	CELZC404	Caenorhabditis elegans	4.70e-05	599	34	0.4	39030	21	CEF41D3	Caenorhabditis elegans	1.11e-05
527	27	0.4	34668	21	CET24H10	Caenorhabditis elegans	1.70e-01	600	31	0.4	39121	21	CEF09C6	Caenorhabditis elegans	7.87e-04
528	27	0.4	34668	21	CET24H10	Caenorhabditis elegans	1.70e-01	601	34	0.4	39211	21	CEC36F7	Caenorhabditis elegans	1.11e-05
529	34	0.4	34700	21	CEC44B9	Caenorhabditis elegans	1.11e-05	602	29	0.4	39235	21	CEL32D1	Caenorhabditis elegans	1.21e-02
530	30	0.4	34700	21	CEC44B9	Caenorhabditis elegans	3.12e-03	603	31	0.4	39271	21	CEF52G2	Caenorhabditis elegans	7.87e-04
531	31	0.4	34759	21	CEC34C12	Caenorhabditis elegans	7.87e-04	604	32	0.4	39271	21	CEF52G2	Caenorhabditis elegans	1.94e-04
532	28	0.4	34775	22	CELW08F4	Caenorhabditis elegans	4.59e-02	605	33	0.4	39273	22	CELK08D9	Caenorhabditis elegans	4.70e-05
533	31	0.4	34841	21	CEC46F11	Caenorhabditis elegans	7.87e-04	606	31	0.4	39337	21	CELB0286	Caenorhabditis elegans	7.87e-04
534	32	0.4	34907	21	CELW01B12	Caenorhabditis elegans	1.94e-04	607	34	0.4	39339	21	CEK08H10	Caenorhabditis elegans	1.11e-05
535	27	0.4	34928	21	CELW01A11	Caenorhabditis elegans	1.70e-01	608	34	0.4	39356	21	CEF32A11	Caenorhabditis elegans	1.11e-05
536	28	0.4	35092	22	CEL21D12	Caenorhabditis elegans	4.59e-02	609	27	0.4	39496	21	CEF13D12	Caenorhabditis elegans	1.70e-01
537	33	0.4	35240	21	CER53	Caenorhabditis elegans	4.70e-05	610	32	0.4	39511	21	CET22C1	Caenorhabditis elegans	1.94e-04
538	31	0.4	35417	21	CELC24G6	Caenorhabditis elegans	7.87e-04	611	27	0.4	39750	21	CEC41C4	Caenorhabditis elegans	4.70e-05
539	27	0.4	35503	21	CEW09D6	Caenorhabditis elegans	1.70e-01	612	28	0.4	39750	21	CEC41C4	Caenorhabditis elegans	7.87e-04
540	27	0.4	35579	22	CELF58B6	Caenorhabditis elegans	1.70e-01	613	34	0.4	39752	22	CELC04F5	Caenorhabditis elegans	4.59e-02
541	27	0.4	35686	22	CELF46E10	Caenorhabditis elegans	1.70e-01	614	27	0.4	39752	22	CELC04F5	Caenorhabditis elegans	1.11e-05
542	29	0.4	35739	21	CEY48A6C	Caenorhabditis elegans	1.21e-02	615	29	0.4	39790	21	CEB0019	Caenorhabditis elegans	1.70e-01
543	32	0.4	35776	21	CELM02G9	Caenorhabditis elegans	4.70e-05	616	27	0.4	39790	21	CEB0019	Caenorhabditis elegans	1.21e-02
544	33	0.4	35782	21	CELF49D11	Caenorhabditis elegans	4.70e-05	617	29	0.4	39902	21	CEE03H4	Caenorhabditis elegans	1.21e-02
545	33	0.4	35850	19	AC006791	Caenorhabditis elegans	4.70e-05	618	29	0.4	39902	21	CEE03H4	Caenorhabditis elegans	1.70e-01
546	31	0.4	35879	21	CEW02A2	Caenorhabditis elegans	7.87e-04	619	27	0.4	39908	21	CEC48D1	Caenorhabditis elegans	4.59e-02
547	31	0.4	35888	21	CET19B10	Caenorhabditis elegans	7.87e-04	620	28	0.4	39931	21	CELC54E4	Caenorhabditis elegans	3.12e-03
548	31	0.4	35985	21	CELF36H9	Caenorhabditis elegans	7.87e-04	621	30	0.4	40090	19	AC006611	Caenorhabditis elegans	3.12e-03
549	33	0.4	35985	21	CELF36H9	Caenorhabditis elegans	4.70e-05	622	30	0.4	40265	21	CEM28	Caenorhabditis elegans	7.87e-04
550	28	0.4	36298	21	CELF25B4	Caenorhabditis elegans	4.59e-02	623	31	0.4	40279	21	CEF56A8	Caenorhabditis elegans	7.87e-04
551	28	0.4	36298	21	CELF25B4	Caenorhabditis elegans	4.59e-02	624	33	0.4	40279	21	CEF56A8	Caenorhabditis elegans	4.70e-05
552	33	0.4	36299	21	CELF25B4	Caenorhabditis elegans	4.70e-05	625	30	0.4	40301	21	CELD1044	Caenorhabditis elegans	3.12e-03
553	34	0.4	36302	21	CEZC482	Caenorhabditis elegans	1.11e-05	626	31	0.4	40453	21	CEC09H10	Caenorhabditis elegans	7.87e-04
554	31	0.4	36355	21	CEM01F1	Caenorhabditis elegans	7.87e-04	627	32	0.4	40457	21	CELF54D7	Caenorhabditis elegans	1.94e-04
555	29	0.4	36355	21	CEM01F1	Caenorhabditis elegans	1.21e-02	628	31	0.4	40553	21	CELF55C5	Caenorhabditis elegans	7.87e-04
556	27	0.4	36400	21	CELF33E11	Caenorhabditis elegans	1.70e-01	629	34	0.4	40553	21	CELF55C5	Caenorhabditis elegans	1.11e-05
557	33	0.4	36404	22	CELD1037	Caenorhabditis elegans	4.70e-05	630	30	0.4	40662	21	CEY32B12B	Caenorhabditis elegans	3.12e-03
558	32	0.4	36490	21	CEF25D7	Caenorhabditis elegans	1.94e-04	631	34	0.4	40780	21	CEM03C11	Caenorhabditis elegans	1.11e-05
559	27	0.4	36524	21	CELF33D4	Caenorhabditis elegans	1.70e-01	632	33	0.4	40912	22	CELC41D11	Caenorhabditis elegans	4.70e-05
560	32	0.4	36532	21	CELF46F11	Caenorhabditis elegans	1.94e-04	633	34	0.4	40912	22	CELC41D11	Caenorhabditis elegans	1.11e-05
561	28	0.4	36749	21	CELM02B7	Caenorhabditis elegans	4.59e-02	634	27	0.4	40921	21	CELB0432	Caenorhabditis elegans	1.70e-01
562	31	0.4	36750	21	CELT15B7	Caenorhabditis elegans	7.87e-04	635	31	0.4	41087	21	CELF09G2	Caenorhabditis elegans	7.87e-04
563	30	0.4	36753	21	CELF19F10	Caenorhabditis elegans	3.12e-03	636	31	0.4	41087	21	CELF09G2	Caenorhabditis elegans	7.87e-04
564	30	0.4	36780	19	CEH10N23	Caenorhabditis elegans	3.12e-03	637	27	0.4	41100	21	CEC31C9	Caenorhabditis elegans	1.94e-04
565	29	0.4	36811	21	CELT20B12	Caenorhabditis elegans	4.59e-02	638	32	0.4	41179	21	CELM01D7	Caenorhabditis elegans	1.94e-04
566	28	0.4	36811	21	CELT20B12	Caenorhabditis elegans	1.21e-02	639	32	0.4	41397	21	CEB0285	Caenorhabditis elegans	1.94e-04
567	29	0.4	36879	19	CEK07H11	Caenorhabditis elegans	1.21e-02	640	33	0.4	41564	21	CELF22F7	Caenorhabditis elegans	1.94e-04
568	29	0.4	36958	21	CEFL1E6	Caenorhabditis elegans	1.21e-02	641	31	0.4	41588	21	CELD1014	Caenorhabditis elegans	7.87e-04
569	34	0.4	36958	21	CEFL1E6	Caenorhabditis elegans	1.11e-05	642	27	0.4	41588	21	CELB0238	Caenorhabditis elegans	1.11e-05
570	28	0.4	36999	21	CELM01B11	Caenorhabditis elegans	4.59e-02	643	34	0.4	41754	21	CELB0238	Caenorhabditis elegans	1.94e-04
571	32	0.4	37037	21	CEFL7C11	Caenorhabditis elegans	1.94e-04	644	32	0.4	41778	21	CELM04G7	Caenorhabditis elegans	7.87e-04
572	34	0.4	37037	21	CEFL7C11	Caenorhabditis elegans	1.11e-05	645	31	0.4	42057	21	CELM09H11	Caenorhabditis elegans	7.87e-04
573	28	0.4	37329	22	CELT19H12	Caenorhabditis elegans	4.59e-02	646	31	0.4	42126	19	AC006834	Caenorhabditis elegans	4.59e-02
574	28	0.4	37342	21	CELC18G1	Caenorhabditis elegans	4.59e-02	647	28	0.4	42171	21	CELC18E3	Caenorhabditis elegans	1.70e-01
575	34	0.4	37353	21	CET12D8	Caenorhabditis elegans	1.11e-05	648	27	0.4	42171	21	CELC18E3	Caenorhabditis elegans	1.11e-05
576	27	0.4	37527	21	CEF22E10	Caenorhabditis elegans	1.70e-01	649	34	0.4	42391	21	CEF28F8	Caenorhabditis elegans	4.70e-05
577	27	0.4	37581	22	CELCZC513	Caenorhabditis elegans	1.70e-01	650	33	0.4	42405	21	CELC18A3	Caenorhabditis elegans	1.94e-04
578	33	0.4	37628	21	CEFL31D4	Caenorhabditis elegans	4.70e-05	651	33	0.4	42426	22	CELC39F7	Caenorhabditis elegans	4.70e-05
579	31	0.4	37635	21	CELK11H12	Caenorhabditis elegans	7.87e-04	652	33	0.4	42472	21	CEC26C6	Caenorhabditis elegans	3.12e-03
580	33	0.4	37635	21	CELK11H12	Caenorhabditis elegans	4.70e-05	653	30	0.4	42472	21	CEC26C6	Caenorhabditis elegans	4.70e-05
581	33	0.4	37854	21	CEC24H11	Caenorhabditis elegans	4.70e-05	654	33	0.4	42521	21	CELC37C3	Caenorhabditis elegans	3.12e-03
582	28	0.4	37881	21	CELK09H9	Caenorhabditis elegans	4.59e-02	655	29	0.4	42521	21	CELC37C3	Caenorhabditis elegans	1.21e-02
583	32	0.4	38092	21	CELT21H3	Caenorhabditis elegans	1.94e-04	656	28	0.4	42703	21	CEC09F9	Caenorhabditis elegans	4.59e-02
584	30	0.4	38103	21	CELR09A1	Caenorhabditis elegans	3.12e-03	657	34	0.4	42724	21	CEF53A2	Caenorhabditis elegans	1.11e-05
585	33	0.4	38119	22	CELD2C	Caenorhabditis elegans	4.70e-05	658	31	0.4	42995	21	CELF31F4	Caenorhabditis elegans	7.87e-04
586	31	0.4	38419	22	CELF23C8	Caenorhabditis elegans	7.87e-04	659	27	0.4	43090	21	CEC08B6	Caenorhabditis elegans	1.70e-01
587	34	0.4	38504	21	CEK13H4	Caenorhabditis elegans	1.11e-05	660	30	0.4	43492	21	CELC14B9	C. elegans cosmid C14B	3.12e-03
588	34	0.4	38523	21	CEK39A1B	Caenorhabditis elegans	1.11e-05	661	34	0.4	43726	21	CELC32E8	Caenorhabditis elegans	1.11e-05
589	28	0.4	38570	21	CELC06A8	Caenorhabditis elegans	4.59e-02	662	32	0.4	44031	19	AC006620	Caenorhabditis elegans	1.94e-04
590	34	0.4	38610	21	CELC18H7	Caenorhabditis elegans	1.11e-05	663	30	0.4	44031	19	AC006620	Caenorhabditis elegans	3.12e-03
591	31	0.4	38681	22	CELR11E3	Caenorhabditis elegans	7.87e-04	664	31	0.4	44090	19	AC006784	Caenorhabditis elegans	7.87e-04
592	29	0.4	38744	21	CEC56A3	Caenorhabditis elegans	1.21e-02	665	31	0.4	44132	22	CELF52C12	Caenorhabditis elegans	7.87e-04
593	28	0.4	38787	21	CET21C12	Caenorhabditis elegans	4.59e-02	666	27	0.4	45348	19	AC006624	Caenorhabditis elegans	1.70e-01
594	30	0.4	38801	19	AC006692	Caenorhabditis elegans	3.12e-03	667	31	0.4	45438	21	CELT05H4	Caenorhabditis elegans	7.87e-04
595	32	0.4	38862	21	CEC06B8	Caenorhabditis elegans	1.94e-04	668	32	0.4	45510	21	CEC32A3	Caenorhabditis elegans	1.94e-04
596	30	0.4	38876	22	CELR119	Caenorhabditis elegans	3.12e-03	669	28	0.4	45510	21	CEC32A3	Caenorhabditis elegans	4.59e-02
597	27	0.4	38984	22	CELF56E10	Caenorhabditis elegans	1.70e-01	670	29	0.4	45713	21	CELB0511	Caenorhabditis elegans	1.21e-02

C	671	34	0.4	47147	21	CELCL6A11	Caenorhabditis elegans	1.11e-05	744	32	0.4	293825	19	CEY48B6	Caenorhabditis elegans	1.94e-04	
C	672	33	0.4	47554	21	CELD1007	Caenorhabditis elegans	4.70e-05	C	745	33	0.4	293825	19	CEY48B6	Caenorhabditis elegans	4.70e-05
C	673	27	0.4	47554	21	CELD1007	Caenorhabditis elegans	1.70e-01	746	33	0.4	294136	20	AC006901	Caenorhabditis elegans	4.70e-05	
C	674	33	0.4	48270	19	CEY43F4	Caenorhabditis elegans	4.70e-05	747	33	0.4	297900	19	AC006704	Caenorhabditis elegans	4.70e-05	
C	675	31	0.4	48270	19	CEY43F4	Caenorhabditis elegans	7.87e-04	748	34	0.4	298216	19	AC006875	Caenorhabditis elegans	1.11e-05	
C	676	34	0.4	48338	19	CET02D9	Caenorhabditis elegans	1.11e-05	C	749	32	0.4	298216	19	AC006875	Caenorhabditis elegans	1.94e-04
C	677	28	0.4	59573	21	CEY45F10D	Caenorhabditis elegans	4.59e-02	750	32	0.4	298406	21	CEY75B8A	Caenorhabditis elegans	1.94e-04	
C	678	30	0.4	66004	21	CEC07A9	Caenorhabditis elegans	3.12e-03	751	29	0.4	298804	19	AC006911	Caenorhabditis elegans	1.94e-04	
C	679	29	0.4	68270	21	CEY7A5A	Caenorhabditis elegans	1.21e-02	C	752	34	0.4	298804	19	AC006911	Caenorhabditis elegans	1.21e-02
C	680	29	0.4	68316	19	CEH16D04	Caenorhabditis elegans	1.21e-02	753	29	0.4	299081	20	AC006892	Caenorhabditis elegans	1.11e-05	
C	681	28	0.4	69430	19	AC006773	Caenorhabditis elegans	4.59e-02	C	754	29	0.4	299081	20	AC006892	Caenorhabditis elegans	1.21e-02
C	682	34	0.4	75342	21	CEY47H9C	Caenorhabditis elegans	1.11e-05	755	33	0.4	299390	20	AC006714	Caenorhabditis elegans	4.70e-05	
C	683	34	0.4	82986	19	CEAA2	Caenorhabditis elegans	1.11e-05	C	756	30	0.4	299390	20	AC006714	Caenorhabditis elegans	3.12e-03
C	684	30	0.4	95968	21	CEY47D3B	Caenorhabditis elegans	3.12e-03	C	757	31	0.4	299427	19	AC006914	Caenorhabditis elegans	7.87e-04
C	685	31	0.4	103725	20	AC006759	Caenorhabditis elegans	7.87e-04	C	758	27	0.4	299427	19	AC006914	Caenorhabditis elegans	1.70e-01
C	686	27	0.4	104180	19	CEZK340	Caenorhabditis elegans	1.70e-01	C	759	30	0.4	299670	19	AC006845	Caenorhabditis elegans	3.12e-03
C	687	34	0.4	108589	19	AC006795	Caenorhabditis elegans	1.11e-05	C	760	30	0.4	299670	19	AC006845	Caenorhabditis elegans	3.12e-03
C	688	32	0.4	108589	19	AC006795	Caenorhabditis elegans	1.94e-04	C	761	31	0.4	299782	19	AC006738	Caenorhabditis elegans	3.12e-03
C	689	33	0.4	108589	19	AC006795	Caenorhabditis elegans	1.94e-04	C	762	27	0.4	300197	19	CEY54G9	Caenorhabditis elegans	7.87e-04
C	690	32	0.4	110000	19	CEY113B8	Caenorhabditis elegans	4.70e-05	C	763	31	0.4	310173	19	CEY62F5	Caenorhabditis elegans	1.70e-01
C	691	31	0.4	110000	19	CEY45F10	Caenorhabditis elegans	1.94e-04	C	764	33	0.4	326074	19	CEY44A6	Caenorhabditis elegans	7.87e-04
C	692	27	0.4	110000	19	CEY38E10	Caenorhabditis elegans	7.87e-04	765	31	0.4	331326	19	AC006802	Caenorhabditis elegans	4.70e-05	
C	693	33	0.4	110000	19	CEY37D8	Caenorhabditis elegans	1.70e-01	C	766	34	0.4	331326	19	AC006802	Caenorhabditis elegans	7.87e-04
C	694	32	0.4	110000	19	CEY45F10	Caenorhabditis elegans	4.70e-05	767	28	0.4	338346	19	CEY87G2	Caenorhabditis elegans	1.11e-05	
C	695	32	0.4	110000	19	CEY116A8	Caenorhabditis elegans	1.94e-04	C	768	33	0.4	338346	19	CEY87G2	Caenorhabditis elegans	4.59e-02
C	696	32	0.4	110000	19	CEY39E4	Caenorhabditis elegans	1.94e-04	C	769	24	0.3	338346	19	CEY87G2	Caenorhabditis elegans	4.70e-05
C	697	27	0.4	110000	19	CEY111B2	Caenorhabditis elegans	1.70e-01	C	770	23	0.3	195	34	HS0612A5	Caenorhabditis elegans	7.19e+00
C	698	29	0.4	117864	19	CEY38G4	Caenorhabditis elegans	1.20e-01	C	771	24	0.3	217	29	HUM276MFD	Homo sapiens DNA sequ	2.35e+01
C	699	34	0.4	117864	19	CEY38G4	Caenorhabditis elegans	1.11e-05	C	772	23	0.3	231	34	AU028624	Rattus norvegicus, OTS	7.19e+00
C	700	30	0.4	119562	19	AC006779	Caenorhabditis elegans	3.12e-03	773	23	0.3	259	34	HS298WE5	H.sapiens (D9S1809) DN	2.35e+01	
C	701	30	0.4	119562	19	AC006779	Caenorhabditis elegans	3.12e-03	774	24	0.3	331	34	HS238XC11	H.sapiens (D18S458) D	2.35e+01	
C	702	27	0.4	126356	19	AC006876	Caenorhabditis elegans	1.70e-01	775	24	0.3	415	23	ECMS2	E. caballus HMS2 micros	7.19e+00	
C	703	28	0.4	129060	21	CEY41C4A	Caenorhabditis elegans	4.59e-02	C	776	24	0.3	603	34	G40453	26580 Zebrafish AB Dan	7.19e+00
C	704	33	0.4	134095	19	AC006915	Caenorhabditis elegans	4.59e-02	C	777	26	0.3	2829	32	MMCCP3	Mouse CCP3 gene for cy	7.19e+00
C	705	29	0.4	134095	19	AC006915	Caenorhabditis elegans	4.70e-05	C	778	24	0.3	3747	19	AC006811	Caenorhabditis elegans	6.09e-01
C	706	27	0.4	141806	20	AC006908	Caenorhabditis elegans	1.21e-02	779	23	0.3	4321	32	MMU66474	Mus musculus preprogra	7.19e+00	
C	707	34	0.4	143092	21	CEY17G7B	Caenorhabditis elegans	1.70e-01	C	779	23	0.3	4906	21	CELUNC60X	Caenorhabditis elegans	2.35e+01
C	708	34	0.4	145614	19	AC006804	Caenorhabditis elegans	1.11e-05	C	780	24	0.3	5017	22	CELE02D9	Caenorhabditis elegans	2.35e+01
C	709	34	0.4	145614	20	AC006872	Caenorhabditis elegans	1.11e-05	C	781	25	0.3	5290	20	AC006886	Caenorhabditis elegans	7.19e+00
C	710	33	0.4	145920	19	AC006710	Caenorhabditis elegans	1.11e-05	782	24	0.3	7035	21	CELCYT1A	Caenorhabditis elegans	2.13e+00	
C	711	33	0.4	152184	19	CEY70G10	Caenorhabditis elegans	4.70e-05	783	25	0.3	7256	22	AF022388	Caenorhabditis elegans	2.13e+00	
C	712	27	0.4	153835	19	CEY6D1	Caenorhabditis elegans	4.70e-05	C	784	26	0.3	7653	21	CELCED3A	Caenorhabditis elegans	6.09e-01
C	713	28	0.4	156152	19	CEY26D4	Caenorhabditis elegans	1.70e-01	C	785	24	0.3	8814	21	CEVT23B5	Caenorhabditis elegans	7.19e+00
C	714	30	0.4	157418	19	AC006912	Caenorhabditis elegans	4.59e-02	C	786	25	0.3	9662	19	AC006775	Caenorhabditis elegans	2.13e+00
C	715	28	0.4	166214	20	AC006735	Caenorhabditis elegans	3.12e-03	787	24	0.3	10169	22	CELH36N01	Caenorhabditis elegans	7.19e+00	
C	716	32	0.4	171817	19	CEY95D11	Caenorhabditis elegans	1.94e-04	C	788	23	0.3	10730	21	CEU28153	Caenorhabditis elegans	2.35e+01
C	717	27	0.4	186306	19	CEY6E2	Caenorhabditis elegans	1.70e-01	C	790	26	0.3	1121				

C	817	23	0.3	26054	21	CELC46A5	Caenorhabditis elegans	2.35e+01	890	25	0.3	36654	21	CEY45F3A	Caenorhabditis elegans	2.13e+00	
C	818	23	0.3	26195	21	CELC04G6	Caenorhabditis elegans	2.35e+01	C	891	25	0.3	36753	21	CELF19F10	Caenorhabditis elegans	2.13e+00
C	819	25	0.3	26283	21	CELF56A3	Caenorhabditis elegans	2.13e+00	C	892	25	0.3	37003	21	CELF33D11	Caenorhabditis elegans	2.13e+00
C	820	26	0.3	26310	21	CELC37A2	Caenorhabditis elegans	6.09e-01	C	893	25	0.3	37310	21	CEZK1098	Caenorhabditis elegans	2.13e+00
C	821	23	0.3	26560	22	CELC07A9	Caenorhabditis elegans	2.35e+01	C	894	23	0.3	37545	21	CETK21C9	Caenorhabditis elegans	2.35e+01
C	822	24	0.3	27394	21	CEFC32B6	Caenorhabditis elegans	7.19e+00	C	895	26	0.3	37634	22	CETK07D4	Caenorhabditis elegans	6.09e-01
C	823	25	0.3	27396	21	CELC54G6	Caenorhabditis elegans	2.13e+00	C	896	25	0.3	37678	21	CELC08B12	Caenorhabditis elegans	2.13e+00
C	824	25	0.3	27540	21	CEZK673	Caenorhabditis elegans	2.13e+00	C	897	24	0.3	37854	21	CEC24H11	Caenorhabditis elegans	7.19e+00
C	825	26	0.3	27567	21	CELT27C4	Caenorhabditis elegans	6.09e-01	C	898	24	0.3	38000	21	CEF58A4	Caenorhabditis elegans	7.19e+00
C	826	23	0.3	27645	21	CELC2K1055	Caenorhabditis elegans	2.35e+01	C	899	25	0.3	38103	21	CELC09A1	Caenorhabditis elegans	2.13e+00
C	827	25	0.3	28026	22	CELY66H1A	Caenorhabditis elegans	2.13e+00	C	900	24	0.3	38463	21	CEK01A6	Caenorhabditis elegans	7.19e+00
C	828	26	0.3	28779	19	AC006824	Caenorhabditis elegans	6.09e-01	C	901	24	0.3	38464	21	CEK08E7	Caenorhabditis elegans	7.19e+00
C	829	24	0.3	28871	21	CEC47B2	Caenorhabditis elegans	7.19e+00	C	902	26	0.3	38464	21	CEK08E7	Caenorhabditis elegans	6.09e-01
C	830	25	0.3	29303	21	CEFC57G4	Caenorhabditis elegans	2.13e+00	C	903	25	0.3	38472	21	CET10E8	Caenorhabditis elegans	2.13e+00
C	831	23	0.3	29739	21	CEC13G3	Caenorhabditis elegans	2.35e+01	C	904	23	0.3	38563	21	CET20B3	Caenorhabditis elegans	2.35e+01
C	832	24	0.3	30415	21	CELM03F8	Caenorhabditis elegans	7.19e+00	C	905	24	0.3	38799	21	CEK04D7	Caenorhabditis elegans	7.19e+00
C	833	25	0.3	30500	21	CER10E12	Caenorhabditis elegans	2.13e+00	C	906	24	0.3	39215	21	CEC1054	Caenorhabditis elegans	7.19e+00
C	834	26	0.3	30969	21	CELT13B5	Caenorhabditis elegans	6.09e-01	C	907	26	0.3	39339	21	CEK08H10	Caenorhabditis elegans	6.09e-01
C	835	25	0.3	31244	21	CEY43F4B	Caenorhabditis elegans	2.13e+00	C	908	23	0.3	39356	21	CEF32A11	Caenorhabditis elegans	2.35e+01
C	836	23	0.3	31261	21	CELF33G12	Caenorhabditis elegans	2.35e+01	C	909	26	0.3	40124	21	CEF09E8	Caenorhabditis elegans	6.09e-01
C	837	25	0.3	31273	21	CEW05E10	Caenorhabditis elegans	2.13e+00	C	910	24	0.3	40145	21	CEC36A4	Caenorhabditis elegans	7.19e+00
C	838	24	0.3	31306	21	CEFC46F3	Caenorhabditis elegans	7.19e+00	C	911	23	0.3	40145	21	CEC36A4	Caenorhabditis elegans	2.35e+01
C	839	26	0.3	31433	21	CELF54C1	Caenorhabditis elegans	6.09e-01	C	912	25	0.3	40202	21	CEC01A2	Caenorhabditis elegans	2.13e+00
C	840	26	0.3	31668	21	CEFC48F5	Caenorhabditis elegans	6.09e-01	C	913	23	0.3	40261	21	CELC17G10	Caenorhabditis elegans	2.35e+01
C	841	24	0.3	31737	21	CELC06B9	Caenorhabditis elegans	7.19e+00	C	914	26	0.3	40301	21	CELD1044	Caenorhabditis elegans	6.09e-01
C	842	23	0.3	31849	21	CELF48A11	Caenorhabditis elegans	2.35e+01	C	915	24	0.3	40359	21	CEC01H6	Caenorhabditis elegans	7.19e+00
C	843	23	0.3	31893	22	CELT22H9	Caenorhabditis elegans	2.35e+01	C	916	25	0.3	40392	21	CEZK1290	Caenorhabditis elegans	2.13e+00
C	844	26	0.3	32009	21	CET06D8	Caenorhabditis elegans	6.09e-01	C	917	26	0.3	40597	21	CEC25A1	Caenorhabditis elegans	6.09e-01
C	845	24	0.3	32009	21	CET06D8	Caenorhabditis elegans	7.19e+00	C	918	23	0.3	40767	21	CEC04F12	Caenorhabditis elegans	2.35e+01
C	846	25	0.3	32096	21	CEFC21A3	Caenorhabditis elegans	2.13e+00	C	919	24	0.3	40873	19	CEH04I09	Caenorhabditis elegans	7.19e+00
C	847	25	0.3	32215	21	CEW02B9	Caenorhabditis elegans	2.13e+00	C	920	24	0.3	41078	22	CELT06A10	Caenorhabditis elegans	7.19e+00
C	848	25	0.3	32243	21	CEW58E10	Caenorhabditis elegans	2.13e+00	C	921	25	0.3	41230	21	CELC14A11	Caenorhabditis elegans	2.13e+00
C	849	24	0.3	32370	21	CEZK669	Caenorhabditis elegans	7.19e+00	C	922	25	0.3	41255	21	CELF56D6	Caenorhabditis elegans	2.13e+00
C	850	24	0.3	32403	21	CELC03B4	Caenorhabditis elegans	7.19e+00	C	923	25	0.3	41452	21	CER06F6	Caenorhabditis elegans	2.13e+00
C	851	26	0.3	32443	22	CEW04C9	Caenorhabditis elegans	6.09e-01	C	924	24	0.3	41498	21	CELB0454	Caenorhabditis elegans	7.19e+00
C	852	24	0.3	32563	22	CELF54D10	Caenorhabditis elegans	7.19e+00	C	925	25	0.3	42057	21	CELC09H11	Caenorhabditis elegans	2.13e+00
C	853	26	0.3	32566	21	CEY94A7B	Caenorhabditis elegans	6.09e-01	C	926	24	0.3	42141	21	CEY54G9A	Caenorhabditis elegans	7.19e+00
C	854	26	0.3	32612	21	CET05D4	Caenorhabditis elegans	6.09e-01	C	927	24	0.3	42223	22	CELF53C3	Caenorhabditis elegans	7.19e+00
C	855	24	0.3	32700	21	CEFC43D9	Caenorhabditis elegans	7.19e+00	C	928	23	0.3	42282	21	CELB0304	Caenorhabditis elegans	2.35e+01
C	856	25	0.3	32703	21	CEFC14D1	Caenorhabditis elegans	2.13e+00	C	929	24	0.3	42528	21	CELB0361	Caenorhabditis elegans	7.19e+00
C	857	23	0.3	32707	21	CELT12F5	Caenorhabditis elegans	2.35e+01	C	930	26	0.3	42861	21	CEFC52B11	Caenorhabditis elegans	6.09e-01
C	858	25	0.3	32723	21	CEM88	Caenorhabditis elegans	2.13e+00	C	931	26	0.3	42912	21	CELM03A1	Caenorhabditis elegans	6.09e-01
C	859	25	0.3	32729	21	CELC05C8	Caenorhabditis elegans	2.13e+00	C	932	24	0.3	43148	21	CEFC52F12	Caenorhabditis elegans	7.19e+00
C	860	25	0.3	32750	21	CELC2K484	Caenorhabditis elegans	2.13e+00	C	933	26	0.3	43526	21	CELC10H11	Caenorhabditis elegans	6.09e-01
C	861	24	0.3	32784	21	CEFC08G5	Caenorhabditis elegans	7.19e+00	C	934	25	0.3	43526	21	CELC10H11	Caenorhabditis elegans	2.13e+00
C	862	26	0.3	32838	21	CELR08F11	Caenorhabditis elegans	6.09e-01	C	935	24	0.3	43589	21	CELC54D2	Caenorhabditis elegans	7.19e+00
C	863	26	0.3	32880	21	CEFC40F12	Caenorhabditis elegans	6.09e-01	C	936	24	0.3	43788	21	CEC10C6	Caenorhabditis elegans	7.19e+00
C	864	23	0.3	33089	21	CEC52E4	Caenorhabditis elegans	2.35e+01	C	937	23	0.3	44090	19	AC006784	Caenorhabditis elegans	2.35e+01
C	865	25	0.3	33089	21	CELT05C3	Caenorhabditis elegans	7.19e+00	C	938	23	0.3	44371	21	CEC47E8	Caenorhabditis elegans	2.35e+01
C	866	24	0.3	33103	21	CEFC31C3	Caenorhabditis elegans	6.09e-01	C	939	26	0.3	44451	21	CELC06E7	Caenorhabditis elegans	6.09e-01
C	867	26	0.3	33164	21	CEFC35C5	Caenorhabditis elegans	6.09e-01	C	940	26	0.3	44686	21	CELC42C1	Caenorhabditis elegans	6.09e-01
C	868	26	0.3	33270	21	CELR02F11	Caenorhabditis elegans	6.09e-01	C	941	24	0.3	44996	21	CEC36B1	Caenorhabditis elegans	7.19e+00
C	869	24	0.3	33330	22	CELF37C12	Caenorhabditis elegans	7.19e+00	C	942	23	0.3	45612	21	CELC35E7	Caenorhabditis elegans	2.35e+01
C	870	25	0.3	33406	21	CEY53C12B	Caenorhabditis elegans	2.13e+00	C	943	24	0.3	47384	21	CELF22E5	Caenorhabditis elegans	7.19e+00
C	871	26	0.3	33478	21	CEFC53B2	Caenorhabditis elegans	6.09e-01	C	944	23	0.3	48173	19	CEY38H8	Caenorhabditis elegans	2.35e+01
C	872	24	0.3	33478	21	CEFC53B2	Caenorhabditis elegans	7.19e+00	C	945	24	0.3	66004	21	CEC07A9	Caenorhabditis elegans	7.19e+00
C	873	25	0.3	33651	21	CELF44E2	C. elegans cosmid F44E	2.13e+00	C	946	26	0.3	70594	19	AC006708	Caenorhabditis elegans	6.09e-01
C	874	26	0.3	34268	21	CEW02D7	Caenorhabditis elegans	6.09e-01	C	947	26	0.3	75073	21	CEY48A6B	Caenorhabditis elegans	6.09e-01
C	875	25	0.3	34766	21	CEW03F8	Caenorhabditis elegans	2.13e+00	C	948	24	0.3	78153	21	CEY53C10A	Caenorhabditis elegans	7.19e+00
C	876	25	0.3	34928	21	CEW01A11	Caenorhabditis elegans	2.13e+00	C	949	23	0.3	82986	19	CEAA2	Caenorhabditis elegans	2.35e+01
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ALIGNMENTS

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ACCESSION L29052
NID 9456416
VERSION L29052.1 GI:456416
KEYWORDS cell death protein; interleukin-1 beta converting enzyme.
SOURCE Caenorhabditis elegans (strain N2) DNA.
ORGANISM Caenorhabditis elegans
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
REFERENCE 1 (bases 1 to 7653)
AUTHORS Yuan, J., Shaham, S., Ledoux, S., Ellis, H.M. and Horvitz, H.
TITLE The C. elegans cell death gene ced-3 encodes a protein similar to mammalian interleukin-1b-converting enzyme
JOURNAL Cell 75, 641-652 (1993)
MEDLINE 94061982
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BASE COUNT 13182 a 6945 c 7146 g 12635 t
ORIGIN

Query Match 54.4%; Score 4164; DB 21; Length 39908;
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3
RESULT CEY67H2 314495 bp DNA HTG 04-MAR-1999
LOCUS Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from
DEFINITION Clone Y67H2, WORKING DRAFT SEQUENCE.
ACCESSION AL022475
NID 94469034
VERSION AL022475.3 GI:4469034
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
REFERENCE Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS 1 (bases 1 to 314495)
TITLE McMurray, A.
JOURNAL Direct Submission
COMMENT Submitted (04-MAR-1999) Nematode Sequencing Project, Sanger Centre,
Hinxtion, Cambridge CB10 1RQ, UK and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rwenematode.wustl.edu
On Mar 22, 1999 this sequence version replaced gi:4468145.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
Location/Qualifiers

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		/chromosome="IV"	
		/clone="Y67H2"	
BASE COUNT	96542 a 54551 c 52760 g 97027 t 13615 others		
ORIGIN			
Query Match	43.9%;	Score 3359;	DB 19; Length 314495;
Best Local Similarity	99.0%;	Pred. NO. 0.00e+00;	
Matches 6209;	Conservative 0;	Mismatches 33;	Indels 31; Gaps 28;
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Db 241400 TTCAGAGAAATGCGTATTACGCAATCATATTTGGCGCGCAAAATATCTCGTAGCTAGAACTA 241459
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Cp 1611 TTCAGAGAAATGCGTATTACAG-TCATATTTGGCGCGCAAAATATCTCGTAGCTAGAACTA 1553
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Db 241460 CAGTACATCTTTAAATGACTACCGTAGCGCTTGTGACGATTTTACGGGTTGTCAAAATTC 241519
|||||
Cp 1552 CAGTA-ATCCTTTAAATGACTACTGTAGCG-TTGTGACGATTTTACGGGTTATCAAAATTC 1495
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Db 241520 GAAAAAATAATTTTCAAAATTTGAGCCGTAATAATCGACACAGCGCTACAGTAGTC 241579
|||||
Cp 1494 GAAAAAATAATTTTCAAAATTTGAGCCGTAATAATCGACACAGCGCTACAGTAGTC 1435
|||||
Db 241580 ATTAAAGAAATTTACTGTAGTTTTCGCTACGAGATATTTTGGCGCTCAAAATATGTTGCGCA 241639
|||||
Cp 1434 ATTAAAGAAATTTACTGTAGTTTTCGCTACGAGATATTTTGC-CGTCAAAATATGTTGCGCA 1376
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Db 241640 GTACGCAATTTCTCAGAAATTTTGTGATTTCTTAAACAGATAATGTCGAGCGGATTTAAAAG- 241698
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Cp 1375 GTACGCAATTTCTCAGAAATTTTGTGATTTCTTAAACAGATAATGTCGAGCGGATTTAAAAG 1316
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Db 241699 A-CTTT-ACCATTTTGTAGTTTTCGGTGTCTATTTATGATAATTTTACGATAAAATTAATA 241756
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Cp 1315 AGCTTTTACCATTTTGTAGTTTTCGGTGTCTATTTATGATAATTTTACGATAAAATTAATA 1256
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Db 241757 CTCAAAAATCGGAATTTTAGCGGAAATATTATAAAAATAAGATGTTAGCACACGAGAGA 241816

Cp 1255 CTCAAAAATCGGAATTTAGCGGAAATATTATAAAAAATAAGATGTTAGCACACGAGAGA 1196
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Db 241817 AAGTCTCGGAAGAAATCATATAACATTTGAGAAGATATTCTTATGGATTGTATATATTGCG 241876
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Cp 1195 AAGTCTCGGAAGAAATCATATAACATTTGAGAAGATATTCTTATGGATTGTATATATTGCG 1136
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Db 241877 TAACAAATTTGGAGAAAGTTTTCGGCCGTTTATTCGCAAAATTTTCGGCGAAAAAAGTTTA 241936
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Cp 1135 TAACAAATTTGGAGAAAGTTTTCGGCCGTTTATTCGCAAAATTTTCGGCGAAAAAAGTTTA 1076
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Db 241937 TGATGGGCTCGTAAGCATGCCGATGAGAAAAAGAAAGTGGATTGTAGCAGCAGCAATATGA 241996
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Cp 1075 TGATGGGCTCGTAAGCATGCCGATGAGAAAAAGAAAGTGGATTGTAGCAGCAGCAATATGA 1016
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Db 241997 GTCACCCATCTGGACAGTTTACATTTCTAAACGATTAATTGAGACGGAG-CAGGTGGCATC 242055
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Cp 1015 GTCACCCATCTGGACAGTTTACATTTCTAAACGATTAATTGAGACGGAGACAGTGGCATC 956
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Db 242056 ACGGAAGAGTGTACCGAAAAACAAACCGGGGCGTTTACCTGAAAGCTCCTGATCTCATC 242115
|||||
Cp 955 ACGGAAGAGTGTACCGAAAAACAAACCGGGGCGTTTACCTGAAAGCTCCTGATCTCATC 896
|||||
Db 242116 AATGATGAAATGTGGTACAAATGAACCGGGCGTTTACCTGAAAGCTCCTGATCTCATC 242175
|||||
Cp 895 AATGATGAAATGTGGTACAAATGAACCGGGCGTTTACCTGAAAGCTCCTGATCTCATC 836
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Db 242176 TAAGATTTCAACCCCGTCATTTGCCTCCATGCACAAATATAATCGGATTTGGATTGTTTA 242235
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Cp 835 TAAGATTTCAACCCCGTCATTTGCCTCCATGCACAAATATAATCGGATTTGGATTGTTTA 776
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Cp 775 AAGCATTGAAATTCGACAAAGAGCTATAAAATCGAAAAAGAGCATACCAAATGAGATACA 716
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Db 242296 CACTGCTTTCTTAAGTGGTTTTCGAAACACACCGCCAAAGAGGTGATGGAGTGGGGSC 242355
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Cp 715 CACTGCTTTCTTAAGTGGTTTTCGAAACACACCGCCAAAGAGGTGATGGAGTGGGGSC 656
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Db 242356 TAAGGAAGAGGTGCGGAGAGGTCAAAATCTTAGGATTTGTTTGTGTTCA 242415
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Cp 655 TAAGGAAGAGGTGCGGAGAGGTCAAAATCTTAGGATTTGTTTGTGTTCA 596
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Db 242416 CATTAATGCGCTCGTAAATTTATTTTGGATTGAGTATCGAAATCTATGAGCCATGA 242475
|||||
Cp 595 CATTAATGCGCTCGTAAATTTATTTTGGATTGAGTATCGAAATCTATGAGCCATGA 536
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Db 242476 ACACGGAGCGGTGAGGTAAAGTTAAAGTTTAAAGTAGTTTATAGTAAACTAATCGT 242535
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Cp 535 ACACGGAGCGGTGAGGTAAAGTTAAAGTTTAAAGTAGTTTATAGTAAACTAATCGT 476
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Db 242536 TTTTCACATAAACAGTGGTTTTTTTAAACGAAAACAATGCAAAACCAAGGTTAAATATTA 242595
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Cp 475 TTTTCACATAAACAGTGGTTTTTTTAAACGAAAACAATGCAAAACCAAGGTTAAATATTA 416
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Db 242596 TAAATCGACTTCGAGAAATCTCAGAAATCTTCTGGCAACAATAAATCGCGAGCCTTTTC 242655
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Cp 415 TAAATCGACTTCGAGAAATCTCAGAAATCTTCTGGCAACAATAAATCGCGAGCCTTTTC 356
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Db 242656 TTCAATTGATGTAATAATGCTTAGCAACACGTTCAACAAAAAGAACAAAAAAGAACG 242715
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Cp 355 TTCAATTGATGTAATAATGCTTAGCAACACGTTCAACAAAAAGAACAAAAAAGAACG 296
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Db 242716 AAAAAAGATGACTGCAAGATAACGGAAAAAGGAG 242748
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Cp 295 AAAAAAGATGACTGCAAGATAACGGAAAAAGGAG 263

RESULT 4 CEY56A3 224746 bp DNA HTG 30-DEC-1998
LOCUS Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from
DEFINITION clone Y56A3, WORKING DRAFT SEQUENCE.
ACCESSION AL022280

NID 94090202
VERSION AL022280.1 GI:4090202
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans

REFERENCE 1 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
AUTHORS Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
TITLE 1 (bases 1 to 224746)
JOURNAL Sulston, J.
Direct Submission
Submitted (30-DEC-1998) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rwenematode.wustl.edu

COMMENT On Dec 31, 1998 this sequence version replaced gi:4006996.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES Location/Qualifiers
source 1..224746
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="III"
/clone="Y56A3"

BASE COUNT 67718 a 40130 c 41166 g 69255 t 6477 others
ORIGIN

Query Match 1.0%; Score 73; DB 19; Length 224746;
Best Local Similarity 100.0%; Pred. No. 1.25e-33;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136606 GCAAAATATCTCGTAGCGAAACTACAGTAATCTTTAAATGACTACTGTAGCGCTTGTG 136665
QY 1394 GCAAAATATCTCGTAGCGAAACTACAGTAATCTTTAAATGACTACTGTAGCGCTTGTG 1453
Db 136666 TCGATTACGGGC 136678
QY 1454 TCGATTACGGGC 1466

RESULT 5
LOCUS AC006766 4917 bp DNA HTG 23-FEB-1999
DEFINITION Caenorhabditis elegans clone Y44E3B, WORKING DRAFT SEQUENCE, 1
unordered pieces.
ACCESSION AC006766
NID 94263172
VERSION AC006766.1 GI:4263172
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans

REFERENCE 1 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
AUTHORS Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
TITLE 1 (bases 1 to 4917)
JOURNAL Waterston, R.H.
The sequence of Caenorhabditis elegans clone
Unpublished
2 (bases 1 to 4917)
REFERENCE Waterston, R.H.
AUTHORS Direct Submission
TITLE Submitted (23-FEB-1999) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT * NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES Location/Qualifiers
source 1..4917
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="Y44E3B"

BASE COUNT 1381 a 977 c 1003 g 1556 t
ORIGIN

Query Match 0.9%; Score 71; DB 19; Length 4917;
Best Local Similarity 100.0%; Pred. No. 4.31e-32;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2646 CCGTAAATCGACACACGCGCTACAGTAGTCATTTAAAGATTACTGTAGTTTCGCTACG 2705
Cp 1464 CCGTAAATCGACACACGCGCTACAGTAGTCATTTAAAGATTACTGTAGTTTCGCTACG 1405
Db 2706 AGATATTTCG 2716
Cp 1404 AGATATTTCG 1394

RESULT 6
LOCUS CELY44E3B 4917 bp DNA INV 05-MAR-1999
DEFINITION Caenorhabditis elegans cosmid Y44E3B.
ACCESSION AF078789
NID 93329615
VERSION AF078789.1 GI:3329615
KEYWORDS
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans

REFERENCE 1 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
AUTHORS Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
TITLE 1 (bases 1 to 4917)
Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifkin, A., Roopra, A.,
Saunders, D., Shownkeen, R., Smalton, N., Smith, A., Sonhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohlman, P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans

TITLE
JOURNAL Nature 368 (6466), 32-38 (1994)
MEDLINE 94150718
REFERENCE 2 (bases 1 to 4917)
AUTHORS Woessner, J., Graves, T. and Keppler, D.
TITLE The sequence of C. elegans cosmid Y44E3B
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 4917)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1998) Department of Genetics, Washington
REFERENCE University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
AUTHORS 4 (bases 1 to 4917)
TITLE Waterston, R.
JOURNAL Direct Submission
REFERENCE 5 (bases 1 to 4917)
AUTHORS Submitted (20-OCT-1998) Department of Genetics, Washington
TITLE University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
JOURNAL 5 (bases 1 to 4917)
REFERENCE Waterston, R.
AUTHORS Direct Submission
TITLE Submitted (05-MAR-1999) Department of Genetics, Washington
JOURNAL University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT

Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
e-mail: rwenematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

This is a segment of YAC Y44E3, sequenced to span the gap between
Y54E10A and W01B11. The 5' clone is Y54E10A; 3' clone is W01B11, 200
bp overlap. Actual start of YAC Y44E3 is at base position 1 of
CELY44E3B; actual end is at 10513 of CELK03E5

NOTES:

Coding sequences below are predicted from computer analysis, using
the program Genefinder(P. Green and L. Hillier, ms in preparation).

FEATURES

source

gene

CDS

1. 4917
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
/clone="Y44E3B"
/chromosome="I"
363. 3080
/gene="Y44E3B.2"
join(363. 637,683. 869,922. 1050,1094. 1166,1220. 1416,
1526. 1629,2867. 3080)
/gene="Y44E3B.2"
/note="contains similarity to the common central domain of
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(Pfam: tyrosinase.hmm, score: 97.33)"
/codon_start=1
/evidence=not_experimental
/protein_id="AAC64634.1"
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/db_xref="GI:3329616"
/translation="MDELHHVFLHTTFNSGSKVNGECYLPSCGKLLKRAVRRLRLSLR
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NPDFGLPFDSTLDSLLPEPKDSIIFSELFLGEVDDKGVKNGPYHNWETMEGRAQIF
RNFGEDDSGEMLDARVDWLINPDINMILGATMPLSTCPMNHITLDARMLFSDHYVH
FFVNGDSKSYSSNDVCFVYHGMIDWIFEHWRQNMOSREERKTEYPKSDERCPPFW
HNGDNSMPLLOPLKNKDALSNGYTDNMYEYPRPTCTRENPDGCDSPYLCFYIPPNNEH
PPSCVSVRRNGVCGFEDYPICYWGQCVDGRCDETVKAPKRLEKFKKFKKIIVPFIM
"

gene

CDS

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/gene="Y44E3B.1"
/note="contains similarity to the basic region plus the
leucine zip domain (Pfam: bZIP.hmm, score: 15.41); coded
for by C. elegans cDNA yk437c3.5; coded for by C. elegans
cDNA yk437c3.3"
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/protein_id="AAC64635.1"
/db_xref="PID:g3329617"
/db_xref="GI:3329617"

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TRRAIKRPSYDDYQEEGETSLSDNDESVDSDSYKPKSKKTAADVFNFPVPTKARKY
NLKPDKEKVEPIYKLKARNNDVARKSRNKAKELOKQKDEYDEMKKRITQLEAELOQS
EREGRERDQQLIKQIREKESTSGPRKSSRNALESFNKSNY"

BASE COUNT 1381 a 977 c 1003 g 1556 t
ORIGIN

Query Match 0.9%; Score 71; DB 22; Length 4917;
Best Local Similarity 100.0%; Pred. No. 4.31e-32;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2646 CCGTAAATCGACACAAAGCGCTACAGTAGTCATTAAAGAAATTAAGTTCGCTACG 2705
|||||

Cp 1464 CCGTAAATCGACACAAAGCGCTACAGTAGTCATTAAAGAAATTAAGTTCGCTACG 1405
|||||

Db 2706 AGATATTTTGC 2716
|||||

Cp 1404 AGATATTTTGC 1394
|||||

RESULT

LOCUS

DEFINITION

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 38846: contig of 38846 bp in length.

FEATURES

source

1. 38846
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="W08E12"

BASE COUNT 11655 a 8013 c 7662 g 11516 t

ORIGIN

Query Match 0.9%; Score 72; DB 19; Length 38846;

Best Local Similarity 100.0%; Pred. No. 7.36e-33;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20039 GAGCCCGTAAATCGACACAAAGCGCTACAGTAGTCATTAAAGAAATTAAGTTCGCTACG 20098
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Cp 1468 GAGCCCGTAAATCGACACAAAGCGCTACAGTAGTCATTAAAGAAATTAAGTTCGCTACG 1409
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Db 20099 TACGAGATATTT 20110
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Cp 1408 TACGAGATATTT 1397
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RESULT 8
LOCUS CEF53A2 42724 bp DNA INV 18-DEC-1998
DEFINITION Caenorhabditis elegans cosmid F53A2, complete sequence.
ACCESSION Z81546
NID 92653125
VERSION 281546.1 GI:2653125
KEYWORDS HTG.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 42724)
Lloyd,C.
Direct Submission
Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rwenematode.wustl.edu
2 (bases 1 to 42724)
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du.Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Showkneen,R., Smaldon,N., Smith,A., Sonhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans
JOURNAL Nature 368 (6466), 32-38 (1994)
MEDLINE 94150718
COMMENT On Nov 29, 1997 this sequence version replaced gi:1914312.
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
For a graphical representation of this sequence and its analysis
see:
http://webace.sanger.ac.uk/cgi-
bin/display?db=wormace&class=Sequence &object=F53A2
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
This sequence is the entire insert of clone F53A2. The start of
this sequence (1..104) overlaps with the end of sequence AL021481.
The end of this sequence (42621..42724) overlaps with the start of
sequence Z99272.
FEATURES
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3023..3189,3624..3748,4327..4705,5046..5115,5241..5385,
5457..5572,5631..5690,6159..6241,6317..6727))
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NEGYNTFMESAECLMELDRKPSVKRCHDETLKEIESANTESGYSVPAKVDKMGALNF
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QGKSVPASPSSILIGCSSINETQVLRIIDCRTSPIPDMLLPTSLHSSSQPHFFTN
FEFTAESLMKCSFTVGKINYGNGSKDSLLPQNEEILQDREPVKVSKYNLFVSYRDMV"
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20302..20427,20612..20778,20834..20923,21567..21648))
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yk403a12.3 comes from this gene; cDNA EST yk403a12.5 comes
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CEESCL8R comes from this gene; cDNA EST CESE72F comes
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from this gene; cDNA EST yk326f9.3 comes from this gene;
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Note: remainder of annotations omitted.

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Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 37750 ATATCTCGTAGCGAAACTACAGTAATCTTTAAATGACTACTGACGCGCTTGTGTCGAT 37809
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QY 1399 ATATCTCGTAGCGAAACTACAGTAATCTTTAAATGACTACTGACGCGCTTGTGTCGAT 1458
Db 37810 TTACGGGCT 37818
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QY 1459 TTACGGGCT 1467

RESULT 9

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DEFINITION
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CEL59B1 43152 bp DNA INV 29-MAY-1998
Caenorhabditis elegans cosmid F59B1.
AF067943
g3165541
AF067943.1 GI:3165541
Caenorhabditis elegans.
Caenorhabditis elegans
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 43152)
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Showkeen,R., Smaldon,N., Smith,A., Sonhammer,E.,
Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans
Nature 368 (6466), 32-38 (1994)
94150718
2 (bases 1 to 43152)
Wu,X.
The sequence of C. elegans cosmid F59B1
Unpublished (1998)
3 (bases 1 to 43152)
Waterston,R.
Direct Submission
Submitted (23-MAY-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

The 5' cosmid is M01F7, 200 bp overlap. Actual start of this
cosmid is at base position 1 of CEL59B1; actual end is at 43152 of
CEL59B1

NOTES:

Coding sequences below are predicted from computer analysis, using
the program Genefinder(P. Green and L. Hillier, ms in preparation).

FEATURES
source

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Note: remainder of annotations omitted.

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RESULT 10
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DEFINITION Caenorhabditis elegans cosmid F59B1.
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NID 93165541
VERSION AF067943.1 GI:3165541
KEYWORDS
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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AUTHORS Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
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Vaughan,K., Waterston,R., Watson,P.
Wilkinson-Sproat,J. and Wohldman,P.
TITLE 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans
JOURNAL Nature 368 (6466), 32-38 (1994)
MEDLINE 94150718
REFERENCE 2 (bases 1 to 43152)
AUTHORS Wu,X.
TITLE The sequence of C. elegans cosmid F59B1
JOURNAL Unpublished (1998)
REFERENCE 3 (bases 1 to 43152)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
e-mail: rwenematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

The 5' cosmid is M01F7, 200 bp overlap. Actual start of this
cosmid is at base position 1 of CELF59B1; actual end is at 43152 of
CELF59B1

NOTES:

Coding sequences below are predicted from computer analysis, using
the program Genefinder(P. Green and L. Hillier, ms in preparation).

FEATURES
Source
1. 43152
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
/clone="F59B1"
/chromosome="v"
complement(2823..3889)

gene

CDS
/gene="F59B1.3"
complement(join(2823..3071,3121..3287,3338..3570,
3617..3780,3827..3889))
/gene="F59B1.3"
/note="contains similarity to seven trans-membrane
receptors (Pfam: 7tm_1.hmm. score: 11.62)"
/codon_start=1
/evidence=not_experimental
/protein_id="AAC17662.1"
/db_xref="PID:g3165545"
/db_xref="GI:3165545"
/translation="MSQEYNYTDPNLVAVFLGTTIGTGVVVCNSLIYVIFLKERSEQ
TAFNVICFFRAISNVIIITFLITPLKTLGLGYSPYPAIESWFINTSHPLYLGNFY
QIVLMAINRFCAMFFPTKYSRIFSLSHTTIILVLIYLRQAQIYEWLPESAKGCYTL
FSTKYFAWKYSSAPGCDYVDGAPEVIKYTFITTAFLNFITFLKILHFYKKSNSQVAV
EAKKMRKNILNFIQTILLDSLYLIDITFTFELRFVDFTILFKHFKQFLEHSPCV
DIFLWNYLGMPTFS"
complement(5565..6879)
/gene="F59B1.5"
complement(join(5565..5727,5810..5844,6104..6270,
6326..6558,6603..6766,6817..6879))
/gene="F59B1.5"
/note="contains similarity to melatonin receptors"
/codon_start=1
/evidence=not_experimental
/protein_id="AAC17665.1"
/db_xref="PID:g3165548"
/db_xref="GI:3165548"
/translation="MSQEYNYTDPNLVAVFLGTTIGTGVVVCNALIYVVFKEKSKR
TAFNVICFFRALSNILITITFLITPLQALLGYSPYPAIESWFINTSNPLYLGNFY
QIVLIAMNRFCAFFPTKYSRIFSLFHTTIIILVLIYLSRQAQIYEWLPWSAKGCYKL
FSTEDFVKYISAPDCDWDVNDAPKIIKYTFIATAILNITFLKILHFYKFLHYFPVD
IFLFIMIIIFNEKIAFLKTKIKKKIVLPITGGGHPRQQTSTVTTSYGNNTFVNN"
complement(8203..10225)
/gene="F59B1.4"
complement(join(8203..8304,8359..8472,8520..8636,
9707..9955,10007..10225))
/gene="F59B1.4"
/codon_start=1
/evidence=not_experimental
/protein_id="AAC17664.1"
/db_xref="PID:g3165547"
/db_xref="GI:3165547"
/translation="MDNRVYATVHLTDRTQLYLTNIFNCLATPVNPLAFYLIKHRS
RETCLKYTLILSHLFYVSNIFYGTIANLLNAFWSAAIWIFLFAFVYFTFMILVV
RLKIVARKGKIFDFSNRSYIFCVILALYIIGPISAIWIRSYCTRDOQIAYVTEHFPK
NLMVFDNPSVHVDSVSNQRMILILMILIFSGFMIYSLLYLMIVLEISKQATSKSLK
TTNHQRKVTNSMVFOILIVGTTVFPAILLQIRNAFVEPEDTRGNIWQ"
complement(12634..14872)
/gene="F59B1.6"
complement(join(12634..12826,13056..13140,13183..13296,
13414..13687,14051..14149,14558..14872))
/gene="F59B1.6"
/note="contains similarity to
NADH-ubiquinone/plastoquinone domains (Pfam:
oxidored_ql.hmm. score: 13.37)"
/codon_start=1
/evidence=not_experimental
/protein_id="AAC17661.1"
/db_xref="PID:g3165544"
/db_xref="GI:3165544"
/translation="MNFVSNSHFFAVIENDRSLQLPLMNLINIVISTIIIVLLYAI
ISRRKKESQIYQIVLITHCFTLWLSQVYWGSHSVFLFPFGLYIGLYLAPFLSSY
VLVIWIFLFAITVTFMILRLRGLRVTRKNSNPFSTTAYSIFSFAFFAMYIAIMP
FCWISAGSSISETQDFVRKYPNATKVLDPGIFVYTDVSKFHRILVVMVLLVSGGV
VSFLKLSQQAAHLHLSMNLNRPAAQMTLERENSKISQKSAERYDYSELTVWHVSC
SNPTFSNSQCIQGRGGHYNHDNHNQNFNCIVNSLRLNLSKHTIQAGCANNVSCS
TQAKCGIDYSSFGSTNLIFKSE"
16526..17717
/gene="F59B1.2"
join(16526..16623,16705..16900,17053..17121,17595..17717)
/gene="F59B1.2"
/codon_start=1
gene
CDS

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/evidence=not_experimental
/protein_id="AAC17663.1"
/db_xref="PID:g3165546"
/db_xref="GI:3165546"
/translation="MYRKTIVLALCALLFVSSIDCKKVKADKKGGKAEEAKVKKVK
AEKIVIVDEPVVHEAAPEVHHAPEVEEAEVWVVKOPVAQKHKISPPKSLKVTSA
FETCKLECRKQDVAQADYVEQLRELASQAALDAENAPVNVNAHHAQAQHVPEVDN
Q"
gene
complement(17869..20354)
/gene="F59B1.7"
complement(join(17869..17933,18236..18503,18667..18842,
18941..19017,19751..19897,19950..20110,20262..20354))
/gene="F59B1.7"
/note="contains similarity to melatonin receptors"
/codon_start=1
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gene

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/evidence=not_experimental
/protein_id="AAC17660.1"
/db_xref="PID:g3165543"
/db_xref="GI:3165543"
/translation="MNDTNGTIAALVEPTVSSQTRFFVTLAIFTISLTGLIGNLSVF
MFATLTKLQNSFGRLSASQSAFAEAVLCGVLEFFYCPMVLDDIPTFKRVSQVGLILL
FCYDVCIFSHLFIENRLCAISFPFIEYNFFMRNTRILALAYAIPTFTSIYMHLAN
NCNLPYDFGWYFVNTSADCDVIRFYVDFCKDFGVVALIAIVDGTIVMIKVTAPGM
KLISANCAQSQKKRREITFVKQALIQGAFATELVEFFIISGMQSQPVAFILCTTVA
WSLVHTIDPLVLLNREFRMLMKNPLTKRTTRVYSITQAIIDNTSSHTN"
complement(25090..31135)
/gene="F59B1.8"
complement(join(25090..25296,25355..25516,25569..25672,
26091..26724,27263..27424,28077..28199,28247..28408,
28463..28566,29655..30312,30980..31135))
/gene="F59B1.8"
/codon_start=1
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gene

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/evidence=not_experimental
/protein_id="AAC17659.1"
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MEVIGDNGFSSRVLLISCNWTIPSAHLPKLLIKIVSFVHIQALIDKGQKNASLIT
KEVEEQMAYAFESSCKMHNQEMNFYEYVAGFNSKTLIPKVFYFTKLDEKNSNKGFI
GMEYVEGSIVRHSYDICTIEEIPIRLAIKQALSQNPAAIESKDLQKIDNGAIFQE
TLKMLLSSEGIKGFIEQCNLRSRFGKEKVDRIEENILDFEKAFNLKVVGIQKN
VLCHGDWAAANFLWTENNGVFCATRIVDYQMSHLGNPAEDLVRLVSTITGADROAHW
QQILEQFYSYFLNELSGEAPYTLQKLSFKLYFPVGLALLPLFGPAVDKLEGM
SEKAEKCRHLKMSKPLSILQPGTGLFNTHVTLFDVNVKAIKEOMSTESLTAESKMEV
IGEGNGFSSCVILITCHWTIPSSHLPKLLIKIVSFVHIQALIDKGQKNASLIT
EAHVHAHEKSCQKHNLEVEFCFAFGHLEGLLPKVFYFTKLDEKNSNKGFI
EGSVVRHCYENVTVDLQPLKALARLQALSSTESCRNLNDNGEAFESLMDLSEDEG
LKGFIDQSRNIDQKLEKVERIEQNHKEILNLETVLNKNVGDIDQKVICHGDLWAAN
ILMTQDGGFIADKVLVDYQESHMGNPAEDLVRLVSTISGADROSHWEHILEQFYTF
TDEIGSNNAPTYTLQKLSFKLYFPVGLALLPLFGPAVDKLEGMESGKAENYRIV
IEKVDCLLDDVLFHDFNKKFTGKN"
32954..34638
gene
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Note: remainder of annotations omitted.

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Query Match      0.9%; Score 72; DB 21; Length 43152;
Best Local Similarity 100.0%; Pred. No. 7.36e-33;
Matches          72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13964 CCCGTAATCGACACAGCGCTACAGTAGTCATTTAAAGAATTACTGTAGTTTCGCTAC 14023
|||||
Cp 1465 CCCGTAATCGACACAGCGCTACAGTAGTCATTTAAAGAATTACTGTAGTTTCGCTAC 1406
|||||
Db 14024 GAGATATTTTC 14035
|||||
Cp 1405 GAGATATTTTC 1394
```

```
RESULT 11
LOCUS CELY44E3A 48088 bp DNA INV 05-MAR-1999
DEFINITION Caenorhabditis elegans cosmid Y44E3A.
ACCESSION AF106589
NID g3886084
```

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AF106589.1 GI:3886084
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 48088)
Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, A., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaildon, N., Smith, A., Sonhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans
Nature 368 (6466), 32-38 (1994)
94150718
2 (bases 1 to 48088)
Woessner, J., Graves, T. and Keppler, D.
The sequence of C. elegans cosmid Y44E3A
Unpublished
3 (bases 1 to 48088)
Waterston, R.
Direct Submission
Submitted (15-NOV-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 48088)
Waterston, R.
Direct Submission
Submitted (05-MAR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:

Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

This segment of YAC Y44E3 was sequenced to span the gap between
W01B11 and W05F2. The 5' clone is W01B11, 200 bp overlap; 3' clone
is W05F2, 2300 bp overlap. Actual start of YAC Y44E3 is at base
position 1 of CELY44E3B; actual end is at 10513 of CELK03E5

NOTES:

Coding sequences below are predicted from computer analysis, using
the program Genefinder(P. Green and L. Hillier, ms in preparation).

FEATURES
source

Location/Qualifiers
1..48088
/organism="Caenorhabditis elegans"
/strain="Bristol N2"


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KEYWORDS      HTG; HTGS_PHASE1.
SOURCE        Caenorhabditis elegans.
ORGANISM      Caenorhabditis elegans
              Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
              Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE     1 (bases 1 to 178553)
AUTHORS       Waterston,R.H.
TITLE         The sequence of Caenorhabditis elegans clone
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 178553)
AUTHORS       Waterston,R.H.
TITLE         Direct Submission
JOURNAL       Submitted (24-FEB-1999) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
COMMENT       * NOTE: This is a 'working draft' sequence. It currently
              * consists of 3 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
              *
              * 1 35017: contig of 35017 bp in length
              * 35018 35031: gap of unknown length
              * 35032 82926: contig of 47895 bp in length
              * 82927 82940: gap of unknown length
              * 82941 178553: contig of 95613 bp in length.
              *
              * Location/Qualifiers
              * 1.178553
              * /organism="Caenorhabditis elegans"
              * /db_xref="taxon:6239"
              * /clone="Y67D8y"
              *
BASE COUNT    54813 a 34476 c 33852 g 55384 t 28 others
ORIGIN

Query Match      0.9%; Score 72; DB 19; Length 178553;
Best Local Similarity 100.0%; Pred. No. 7.36e-33;
Matches          72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126055 GAGCCGTAATCGACACACGCGCTACAGTAGTCATTTAAAGAAATTACTGTAGTTTCGC 126114
|||||
Cp 1468 GAGCCGTAATCGACACACGCGCTACAGTAGTCATTTAAAGAAATTACTGTAGTTTCGC 1409
|||||

Db 126115 TACGAGATATT 126126
|||||
Cp 1408 TACGAGATATT 1397
|||||

RESULT 13
LOCUS      AC006752 245805 bp DNA HTG 25-FEB-1999
DEFINITION Caenorhabditis elegans clone Y39H10, WORKING DRAFT SEQUENCE, 6
            unordered pieces.
ACCESSION  AC006752
NID        g4309798
VERSION    AC006752.2 GI:4309798
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE  1 (bases 1 to 245805)
AUTHORS    Waterston,R.H.
TITLE      The sequence of Caenorhabditis elegans clone
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 245805)
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (23-FEB-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT    * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 2691: contig of 2691 bp in length
            * 2692 2706: gap of unknown length
            * 2707 5448: contig of 2742 bp in length
            * 5449 5463: gap of unknown length
            * 5464 14405: contig of 8942 bp in length
            * 14406 14420: gap of unknown length
            * 14421 28085: contig of 13665 bp in length
            * 28086 28100: gap of unknown length
            * 28101 84320: contig of 56220 bp in length
            * 84321 84335: gap of unknown length
            * 84336 245805: contig of 161470 bp in length.
            *
            * Location/Qualifiers
            * 1.245805
            * /organism="Caenorhabditis elegans"
            * /db_xref="taxon:6239"
            * /clone="Y39H10"
            *
BASE COUNT    77112 a 45383 c 45498 g 77737 t 75 others
ORIGIN

Query Match      0.9%; Score 72; DB 20; Length 245805;
Best Local Similarity 100.0%; Pred. No. 7.36e-33;
Matches          72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 193263 GCAAAATATCTCGTAGCGAAACACAGTAATCTTTAAATGACTACTGTAGCGCTTGTG 193322
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QY 1394 GCAAAATATCTCGTAGCGAAACACAGTAATCTTTAAATGACTACTGTAGCGCTTGTG 1453
|||||

Db 193323 TCGATTACGGG 193334
|||||
QY 1454 TCGATTACGGG 1465
|||||

RESULT 14
LOCUS      AC006752 245805 bp DNA HTG 25-FEB-1999
DEFINITION Caenorhabditis elegans clone Y39H10, WORKING DRAFT SEQUENCE, 6
            unordered pieces.
ACCESSION  AC006752
NID        g4309798
VERSION    AC006752.2 GI:4309798
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     Caenorhabditis elegans.
ORGANISM   Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE  1 (bases 1 to 245805)
AUTHORS    Waterston,R.H.
TITLE      The sequence of Caenorhabditis elegans clone
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 245805)
AUTHORS    Waterston,R.H.
TITLE      Direct Submission
JOURNAL    Submitted (23-FEB-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT    * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 2691: contig of 2691 bp in length
            * 2692 2706: gap of unknown length
            * 2707 5448: contig of 2742 bp in length
            * 5449 5463: gap of unknown length
            * 5464 14405: contig of 8942 bp in length
            * 14406 14420: gap of unknown length
            * 14421 28085: contig of 13665 bp in length
            * 28086 28100: gap of unknown length
            * 28101 84320: contig of 56220 bp in length
            * 84321 84335: gap of unknown length
            * 84336 245805: contig of 161470 bp in length.
            *
            * Location/Qualifiers
            * 1.245805
            * /organism="Caenorhabditis elegans"
            * /db_xref="taxon:6239"
            * /clone="Y39H10"
            *
BASE COUNT    77112 a 45383 c 45498 g 77737 t 75 others
ORIGIN
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* 5449 5463: gap of unknown length
* 5464 14405: contig of 8942 bp in length
* 14406 14420: gap of unknown length
* 14421 28085: contig of 13665 bp in length
* 28086 28100: gap of unknown length
* 28101 84320: contig of 56220 bp in length
* 84321 84335: gap of unknown length
* 84336 245805: contig of 161470 bp in length.

FEATURES
source
1. .245805
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="Y39H10"
77112 a 45383 c 45498 g 77737 t 75 others

Query Match 0.9%; Score 72; DB 20; Length 245805;
Best Local Similarity 100.0%; Pred. No. 7.36e-33;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 193472 CCGTAATTCGACACACGCTACAGTAGTCATTAAAGAAATTAAGTATGTTTCGCTAC 193531
|||||
Cp 1465 CCGTAATTCGACACACGCTACAGTAGTCATTAAAGAAATTAAGTATGTTTCGCTAC 1406

Db 193532 GAGATATTTGTC 193543

Cp 1405 GAGATATTTGTC 1394

RESULT 15 AC006890 298195 bp DNA HTG 24-FEB-1999
LOCUS Caenorhabditis elegans clone Y67D8x, WORKING DRAFT SEQUENCE, 23
DEFINITION unorderd pieces.
ACCESSION AC006890
NID g4263458
VERSION AC006890.1 GI:4263458
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 298195)
Waterston,R.H.
The sequence of Caenorhabditis elegans clone

REFERENCE 2 (bases 1 to 298195)
AUTHORS Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 298195)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2711: contig of 2711 bp in length
* 2712 2725: gap of unknown length
* 2726 5159: contig of 2434 bp in length
* 5160 5173: gap of unknown length
* 5174 7175: contig of 2002 bp in length
* 7176 7189: gap of unknown length
* 7190 9231: contig of 2042 bp in length
* 9232 9245: gap of unknown length
* 9246 13485: contig of 4240 bp in length
* 13486 13499: gap of unknown length
* 13500 17911: contig of 4412 bp in length
* 17912 17925: gap of unknown length
* 17926 25108: contig of 7183 bp in length
* 25109 25122: gap of unknown length

* 25123 32230: contig of 7108 bp in length
* 32231 32244: gap of unknown length
* 32245 37881: contig of 5637 bp in length
* 37882 37895: gap of unknown length
* 37896 45252: contig of 7357 bp in length
* 45253 45266: gap of unknown length
* 45267 55076: contig of 9810 bp in length
* 55077 55090: gap of unknown length
* 55091 64617: contig of 9527 bp in length
* 64618 64631: gap of unknown length
* 64632 75764: contig of 11133 bp in length
* 75765 75778: gap of unknown length
* 75779 94579: contig of 18801 bp in length
* 94580 94593: gap of unknown length
* 94594 109448: contig of 14855 bp in length
* 109449 109462: gap of unknown length
* 109463 124264: contig of 14802 bp in length
* 124265 124278: gap of unknown length
* 124279 141464: contig of 17186 bp in length
* 141465 141478: gap of unknown length
* 141479 161525: contig of 20047 bp in length
* 161526 161539: gap of unknown length
* 161540 181163: contig of 19624 bp in length
* 181164 181177: gap of unknown length
* 181178 206333: contig of 25156 bp in length
* 206334 206347: gap of unknown length
* 206348 253285: contig of 46938 bp in length
* 253286 253299: gap of unknown length
* 253300 283961: contig of 30662 bp in length
* 283962 283975: gap of unknown length
* 283976 298195: contig of 14220 bp in length.

FEATURES
source
1. .298195
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="Y67D8x"

BASE COUNT 94617 a 53720 c 56055 g 93495 t 308 others
ORIGIN

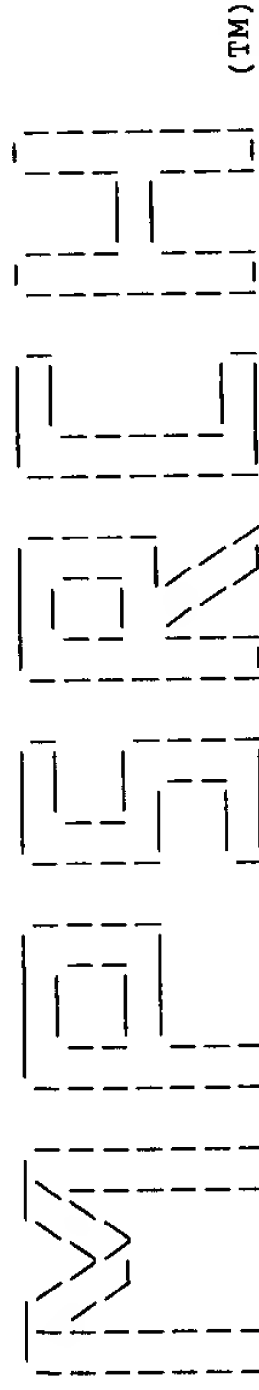
Query Match 0.9%; Score 72; DB 19; Length 298195;
Best Local Similarity 100.0%; Pred. No. 7.36e-33;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 64506 AAATATCTCGTAGCGAAACTACAGTAATTTAAATGACTACTGTGTCG 64565
|||||
Qy 1397 AAATATCTCGTAGCGAAACTACAGTAATTTAAATGACTACTGTGTCG 1456

Db 64566 ATTTACGGGCTC 64577

Qy 1457 ATTTACGGGCTC 1468

Search completed: Sun Aug 8 20:50:23 1999
Job time : 13725 secs.



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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Mon Aug 9 00:23:43 1999; MasPar time 1622.43 Seconds
Tabular output not generated. 1010.719 Million cell updates/sec

Title: >US-08-287-669-18
Description: (1-7653) from US08287669.seq (10 of 10)
Perfect Score: 7653
N.A. Sequence: 1 AGATCTGAATAAGTGATA.....ATTCTGGTCAGCAAGATCT 7653
Comp: TCTAGACTTTATCCACTAT.....TAAGACCAGTCGTTCTAGA

Scoring table: TABLE jmetric
Gap 60

Nmatch STD : Dbase 0; Query 0

Searched: 271905 seqs, 107135622 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database: n-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 9.051; Variance 3.852; scale 2.350

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	7622	99.6	7653	24	T38196 Nematode Ced-3 gene.	0.00e+00
2	7405	96.8	7653	9	Q54401 ced-3 gene.	0.00e+00
3	7219	94.3	7653	9	Q54666 ced-3 gene.	0.00e+00
4	7126	93.1	7653	9	Q64741 ced-3 (G6372A) gene.	0.00e+00
5	7126	93.1	7653	9	Q64742 ced-3 (G6434T) gene.	0.00e+00
6	7126	93.1	7653	9	Q64744 ced-3 (G6536A) gene.	0.00e+00
7	7126	93.1	7653	9	Q64743 ced-3 (C6485T) gene.	0.00e+00
8	7126	93.1	7653	9	Q64740 ced-3 (C6322T) gene.	0.00e+00
9	7126	93.1	7653	9	Q64737 ced-3 (G5757A) gene.	0.00e+00

10	7126	93.1	7653	9	Q64745	ced-3 (C7020T) gene.	0.00e+00
11	7126	93.1	7653	9	Q64736	ced-3 (G2487A) gene.	0.00e+00
12	7126	93.1	7653	9	Q64739	ced-3 (G6297A) gene.	0.00e+00
13	7126	93.1	7653	9	Q64738	ced-3 (C5940T) gene.	0.00e+00
14	505	6.6	2485	14	Q79970	Interleukin-1 beta co	0.00e+00
15	39	0.5	6560	9	Q54629	Genomic region contai	1.18e-13
16	30	0.4	30	9	Q54668	ced-3 gene primer Pex	9.66e-07
17	30	0.4	30	24	T38198	Nematode Ced-3 gene p	9.66e-07
18	30	0.4	30	24	T38199	Nematode Ced-3 gene p	9.66e-07
19	30	0.4	30	9	Q54667	ced-3 gene primer Pex	9.66e-07
20	30	0.4	30	22	T31559	PCR primer Pex1 for c	9.66e-07
21	30	0.4	30	22	T31560	PCR primer Pex2 for c	9.66e-07
22	21	0.3	146	49	V48134	Z-chromosomal microsa	1.28e+00
23	21	0.3	183	53	V89661	EST clone DA165.	1.28e+00
24	20	0.3	216	49	V48146	Z-chromosomal microsa	5.14e+00
25	22	0.3	240	29	T65683	Polymorphic repeat se	3.04e-01
26	20	0.3	305	10	Q55239	Grapevine ribosomal c	5.14e+00
27	21	0.3	324	53	V89077	EST clone BZ87.	1.28e+00
28	21	0.3	474	49	V48133	Z-chromosomal microsa	5.14e+00
29	21	0.3	534	30	T43947	Sequence flanking mar	1.28e+00
30	21	0.3	534	30	T72067	Sequence flanking mar	1.28e+00
31	21	0.3	1107	11	Q68716	GDI D4 cDNA.	1.28e+00
32	20	0.3	1413	29	T67416	H. pylori cytoplasmic	5.14e+00
33	20	0.3	1729	13	Q75336	Superoxide-dismutase-	5.14e+00
34	20	0.3	1910	51	V59790	Human secreted protei	5.14e+00
35	20	0.3	1945	51	V59664	Human secreted protei	5.14e+00
36	20	0.3	2001	60	X13129	Enterococcus faecalis	5.14e+00
37	20	0.3	2101	32	T72896	Plasmodium ebl-2 gene	5.14e+00
38	20	0.3	2101	14	Q83528	P. falciparum EBL-e2	5.14e+00
39	21	0.3	2269	15	Q97244	Rat AT1 cDNA.	1.28e+00
40	20	0.3	2347	24	T39541	Mouse receptor 4-1BB	5.14e+00
41	20	0.3	2347	24	T39541	Mouse receptor 4-1BB	5.14e+00
42	20	0.3	2350	14	Q86127	4-1BB receptor protei	5.14e+00
43	21	0.3	2350	14	Q86127	4-1BB receptor protei	5.14e+00
44	20	0.3	2772	3	Q20670	Diacylglycerol kinas	5.14e+00
45	20	0.3	2875	29	T47713	Mouse bone morphogene	5.14e+00
46	21	0.3	3825	29	T33962	Mutated beta-amylose	1.28e+00
47	21	0.3	3825	29	T33961	Beta-amylose coding s	1.28e+00
48	20	0.3	4185	47	V52306	Streptococcus pneumon	5.14e+00
49	20	0.3	5438	5	Q29263	Human calcium channel	5.14e+00
50	24	0.3	6560	9	Q54629	Genomic region contai	1.54e-02
51	20	0.3	7107	60	X13464	Enterococcus faecalis	5.14e+00
52	20	0.3	7295	32	T72883	Plasmodium var-1 gene	5.14e+00
53	26	0.3	7653	9	Q64744	ced-3 (G6536A) gene.	6.81e-04
54	26	0.3	7653	9	Q64736	ced-3 (G2487A) gene.	6.81e-04
55	26	0.3	7653	9	Q64739	ced-3 (G6297A) gene.	6.81e-04
56	26	0.3	7653	9	Q64743	ced-3 (C6485T) gene.	6.81e-04
57	26	0.3	7653	9	Q64737	ced-3 (G5757A) gene.	6.81e-04
58	26	0.3	7653	24	T38196	Nematode Ced-3 gene.	6.81e-04
59	26	0.3	7653	9	Q54666	ced-3 gene.	6.81e-04
60	26	0.3	7653	9	Q64745	ced-3 (C7020T) gene.	6.81e-04
61	26	0.3	7653	9	Q64740	ced-3 (C6322T) gene.	6.81e-04
62	26	0.3	7653	9	Q64741	ced-3 (G6372A) gene.	6.81e-04
63	26	0.3	7653	9	Q54401	ced-3 gene.	6.81e-04
64	26	0.3	7653	9	Q64742	ced-3 (C6434T) gene.	6.81e-04
65	26	0.3	7653	9	Q64738	ced-3 (C5940T) gene.	6.81e-04
66	20	0.3	13104	8	Q46852	Clone of recombinant	5.14e+00
67	20	0.3	15144	29	T47715	Mouse bone morphogene	5.14e+00
68	20	0.3	116624	48	V52850	Human eyal gene conti	5.14e+00
69	20	0.3	116624	48	V52850	Human eyal gene conti	5.14e+00
70	21	0.3	235033	51	V57926	Hereditary haemochrom	1.28e+00
71	21	0.3	237326	50	V57903	Hereditary haemochrom	1.28e+00
72	20	0.3	580073	27	T58840	Mycoplasma genitalium	5.14e+00
73	18	0.2	18	7	Q46588	Simple sequence repea	7.21e+01
74	18	0.2	18	5	Q33950	Sequence of a microsa	7.21e+01
75	18	0.2	18	5	Q33950	Microsatellite sequen	7.21e+01
76	18	0.2	19	2	T66093	Repeat sequence found	7.21e+01
77	19	0.2	19	14	Q79978	Interleukin-1 beta co	1.97e+01
78	19	0.2	19	24	T38202	Nematode Ced-3 gene p	1.97e+01
79	19	0.2	19	22	T31562	PCR primer log-5 for	1.97e+01
80	19	0.2	19	9	Q54671	ced-3 gene primer Log	1.97e+01
81	18	0.2	19	5	Q33728	Microsatellite sequen	7.21e+01
82	18	0.2	20	35	T93829	Antitumoural phosphod	7.21e+01

ced-3 (C7020T) gene.
ced-3 (G2487A) gene.
ced-3 (G6297A) gene.
ced-3 (C5940T) gene.
Interleukin-1 beta co
Genomic region contai
ced-3 gene primer Pex
Nematode Ced-3 gene p
Nematode Ced-3 gene p
ced-3 gene primer Pex
PCR primer Pex1 for c
PCR primer Pex2 for c
Z-chromosomal microsa
EST clone DA165.
Z-chromosomal microsa
Polymorphic repeat se
Grapevine ribosomal c
EST clone BZ87.
Z-chromosomal microsa
Sequence flanking mar
Sequence flanking mar
GDI D4 cDNA.
H. pylori cytoplasmic
Superoxide-dismutase-
Human secreted protei
Human secreted protei
Enterococcus faecalis
Plasmodium ebl-2 gene
P. falciparum EBL-e2
Rat AT1 cDNA.
Mouse receptor 4-1BB
Mouse receptor 4-1BB
4-1BB receptor protei
4-1BB receptor protei
Diacylglycerol kinas
Mouse bone morphogene
Mutated beta-amylose
Beta-amylose coding s
Streptococcus pneumon
Human calcium channel
Genomic region contai
Enterococcus faecalis
Plasmodium var-1 gene
ced-3 (G6536A) gene.
ced-3 (G2487A) gene.
ced-3 (G6297A) gene.
ced-3 (C6485T) gene.
ced-3 (G5757A) gene.
Nematode Ced-3 gene.
ced-3 gene.
ced-3 (C7020T) gene.
ced-3 (C6322T) gene.
ced-3 (G6372A) gene.
ced-3 gene.
ced-3 (C6434T) gene.
ced-3 (C5940T) gene.
Clone of recombinant
Mouse bone morphogene
Human eyal gene conti
Human eyal gene conti
Hereditary haemochrom
Hereditary haemochrom
Mycoplasma genitalium
Simple sequence repea
Sequence of a microsa
Microsatellite sequen
Repeat sequence found
Interleukin-1 beta co
Nematode Ced-3 gene p
PCR primer log-5 for
ced-3 gene primer Log
Microsatellite sequen
Antitumoural phosphod

83	18	0.2	20	5	Q33816	Microsatellite sequen	7.21e+01	156	18	0.2	32	29	T65752	Repeat sequence from	7.21e+01
84	18	0.2	20	5	Q33672	Microsatellite sequen	7.21e+01	157	18	0.2	32	29	T66057	(dC-dA)n.(dG-dT)n pol	7.21e+01
85	18	0.2	20	5	Q34170	Sequence of a microsa	7.21e+01	158	18	0.2	32	29	T65790	Repeat sequence from	7.21e+01
86	18	0.2	20	41	V06824	Oligonucleotide which	7.21e+01	159	18	0.2	32	5	Q34149	Sequence of a microsa	7.21e+01
87	18	0.2	20	9	Q49455	Primer for detecting	7.21e+01	160	18	0.2	32	5	Q34119	Sequence of a microsa	7.21e+01
88	18	0.2	21	29	T65738	Repeat sequence from	7.21e+01	161	19	0.2	33	29	T65770	Repeat sequence from	1.97e+01
89	18	0.2	21	5	Q33891	Microsatellite sequen	7.21e+01	162	18	0.2	33	29	T65705	Repeat sequence from	7.21e+01
90	18	0.2	21	5	Q33879	Microsatellite sequen	7.21e+01	163	19	0.2	33	5	Q33731	Microsatellite sequen	1.97e+01
91	18	0.2	22	29	T65727	Repeat sequence from	7.21e+01	164	18	0.2	33	5	Q34009	Microsatellite sequen	7.21e+01
92	18	0.2	22	14	Q83952	Oligonucleotide clamp	7.21e+01	165	18	0.2	33	5	Q33944	Microsatellite sequen	7.21e+01
93	19	0.2	22	5	Q33716	Microsatellite sequen	1.97e+01	166	18	0.2	33	5	Q34097	Sequence of a microsa	7.21e+01
94	18	0.2	22	5	Q34038	Microsatellite sequen	7.21e+01	167	18	0.2	34	29	T65742	Repeat sequence from	7.21e+01
95	18	0.2	22	5	Q33675	Microsatellite sequen	7.21e+01	168	18	0.2	34	29	T65744	Repeat sequence from	7.21e+01
96	18	0.2	22	5	Q33810	Microsatellite sequen	7.21e+01	169	18	0.2	34	29	T65748	Repeat sequence from	7.21e+01
97	18	0.2	22	5	Q34080	Microsatellite sequen	7.21e+01	170	18	0.2	34	29	T65722	Repeat sequence from	7.21e+01
98	18	0.2	22	5	Q33991	Microsatellite sequen	7.21e+01	171	18	0.2	34	29	T65772	Repeat sequence from	7.21e+01
99	18	0.2	22	5	Q33888	Microsatellite sequen	7.21e+01	172	18	0.2	34	5	Q33924	Repeat sequence from	7.21e+01
100	18	0.2	23	29	T66105	Repeat sequence found	7.21e+01	173	18	0.2	34	5	Q33921	Microsatellite sequen	7.21e+01
101	18	0.2	23	5	Q33773	Microsatellite sequen	7.21e+01	174	18	0.2	34	5	Q33921	Microsatellite sequen	7.21e+01
102	18	0.2	23	5	Q33663	Microsatellite sequen	7.21e+01	175	18	0.2	34	5	Q33873	Microsatellite sequen	7.21e+01
103	18	0.2	23	5	Q33885	Microsatellite sequen	7.21e+01	176	18	0.2	34	5	Q33776	Microsatellite sequen	7.21e+01
104	18	0.2	24	29	T66096	Repeat sequence found	7.21e+01	177	18	0.2	34	5	Q33734	Microsatellite sequen	7.21e+01
105	18	0.2	24	5	Q34158	Sequence of a microsa	7.21e+01	178	18	0.2	34	5	Q33692	Microsatellite sequen	7.21e+01
106	18	0.2	24	5	Q33707	Microsatellite sequen	7.21e+01	179	18	0.2	35	29	T65747	Repeat sequence from	7.21e+01
107	18	0.2	24	5	Q34024	Microsatellite sequen	7.21e+01	180	18	0.2	35	5	T65711	Repeat sequence from	7.21e+01
108	18	0.2	24	5	Q33986	Microsatellite sequen	7.21e+01	181	18	0.2	35	5	Q33695	Microsatellite sequen	7.21e+01
109	18	0.2	24	5	Q33909	Microsatellite sequen	7.21e+01	182	18	0.2	35	5	Q33713	Microsatellite sequen	7.21e+01
110	18	0.2	25	29	T65734	Repeat sequence from	7.21e+01	183	18	0.2	35	5	Q34021	Microsatellite sequen	7.21e+01
111	18	0.2	25	5	Q33861	Microsatellite sequen	7.21e+01	184	18	0.2	36	14	Q83935	Oligonucleotide clamp	7.21e+01
112	18	0.2	25	5	Q33918	Microsatellite sequen	7.21e+01	185	18	0.2	36	29	T65720	Repeat sequence from	7.21e+01
113	18	0.2	25	5	Q33962	Microsatellite sequen	7.21e+01	186	18	0.2	36	29	T65784	Repeat sequence from	7.21e+01
114	18	0.2	25	5	Q33642	Microsatellite sequen	7.21e+01	187	19	0.2	36	5	Q34107	Sequence of a microsa	1.97e+01
115	18	0.2	25	5	Q33704	Microsatellite sequen	7.21e+01	188	18	0.2	36	5	Q33828	Microsatellite sequen	7.21e+01
116	18	0.2	26	5	Q33684	Microsatellite sequen	7.21e+01	189	18	0.2	36	5	Q33882	Microsatellite sequen	7.21e+01
117	18	0.2	26	5	Q34016	Microsatellite sequen	7.21e+01	190	18	0.2	36	5	Q33819	Microsatellite sequen	7.21e+01
118	18	0.2	26	7	Q44016	Target sequence #8	7.21e+01	191	18	0.2	36	5	Q33953	Microsatellite sequen	7.21e+01
119	18	0.2	26	5	Q33837	Microsatellite sequen	7.21e+01	192	18	0.2	36	5	Q33974	Microsatellite sequen	7.21e+01
120	18	0.2	26	7	Q47179	MHC DR A intron bindi	7.21e+01	193	18	0.2	36	5	Q34152	Sequence of a microsa	7.21e+01
121	18	0.2	26	5	Q34083	Microsatellite sequen	7.21e+01	194	18	0.2	36	5	Q34068	Microsatellite sequen	7.21e+01
122	18	0.2	26	5	Q33831	Microsatellite sequen	7.21e+01	195	18	0.2	36	5	Q33906	Microsatellite sequen	7.21e+01
123	18	0.2	27	14	Q95132	Microsatellite sequen	7.21e+01	196	19	0.2	37	5	Q33698	Microsatellite sequen	7.21e+01
124	18	0.2	27	29	T65733	Spinocerebellar ataxi	7.21e+01	197	18	0.2	37	5	Q33900	Microsatellite sequen	1.97e+01
125	19	0.2	27	14	Q83951	Repeat sequence from	7.21e+01	198	18	0.2	37	5	Q34184	Microsatellite sequen	7.21e+01
126	18	0.2	27	5	Q34077	Oligonucleotide clamp	7.21e+01	199	18	0.2	37	5	Q33710	Microsatellite sequen	7.21e+01
127	18	0.2	27	5	Q34181	Microsatellite sequen	1.97e+01	200	18	0.2	37	5	Q34041	Microsatellite sequen	7.21e+01
128	18	0.2	27	5	Q33678	Microsatellite sequen	7.21e+01	201	18	0.2	37	5	Q34178	Microsatellite sequen	7.21e+01
129	18	0.2	27	14	Q95129	Spinocerebellar ataxi	7.21e+01	202	18	0.2	38	29	T66048	(dC-dA)n.(dG-dT)n pol	7.21e+01
130	18	0.2	27	5	Q34143	Sequence of a microsa	7.21e+01	203	18	0.2	38	29	T65750	Repeat sequence from	7.21e+01
131	18	0.2	27	5	Q33804	Microsatellite sequen	7.21e+01	204	18	0.2	38	10	Q68850	Human chromosomal rep	7.21e+01
132	18	0.2	27	5	Q34044	Microsatellite sequen	7.21e+01	205	18	0.2	38	29	T65708	Repeat sequence from	7.21e+01
133	18	0.2	27	5	Q34012	Microsatellite sequen	7.21e+01	206	18	0.2	38	5	Q33767	Microsatellite sequen	7.21e+01
134	18	0.2	28	29	T66102	Repeat sequence found	7.21e+01	207	18	0.2	38	5	Q33894	Microsatellite sequen	7.21e+01
135	18	0.2	28	5	Q33933	Microsatellite sequen	7.21e+01	208	19	0.2	39	29	T65714	Repeat sequence from	1.97e+01
136	18	0.2	28	5	Q33645	Microsatellite sequen	7.21e+01	209	18	0.2	39	29	T65775	Repeat sequence from	7.21e+01
137	18	0.2	28	4	Q34000	Microsatellite sequen	7.21e+01	210	18	0.2	39	29	T65731	Repeat sequence from	7.21e+01
138	18	0.2	28	5	Q34035	Microsatellite sequen	7.21e+01	211	18	0.2	39	5	Q33737	Microsatellite sequen	1.97e+01
139	18	0.2	28	5	Q34027	Microsatellite sequen	7.21e+01	212	18	0.2	39	5	Q33807	Microsatellite sequen	7.21e+01
140	18	0.2	28	5	Q34161	Sequence of a microsa	7.21e+01	213	18	0.2	39	5	Q33825	Microsatellite sequen	7.21e+01
141	18	0.2	29	29	T65712	Repeat sequence from	7.21e+01	214	19	0.2	40	24	T27907	Compound in phase sim	1.97e+01
142	18	0.2	29	14	Q83953	Oligonucleotide clamp	7.21e+01	215	18	0.2	40	29	T65743	Repeat sequence from	1.97e+01
143	18	0.2	29	29	T65760	Repeat sequence from	7.21e+01	216	18	0.2	40	29	T66054	(dC-dA)n.(dG-dT)n pol	7.21e+01
144	18	0.2	29	5	Q33977	Microsatellite sequen	7.21e+01	217	18	0.2	40	29	T65736	Repeat sequence from	7.21e+01
145	18	0.2	29	5	Q33687	Microsatellite sequen	7.21e+01	218	18	0.2	40	29	T66051	(dC-dA)n.(dG-dT)n pol	7.21e+01
146	18	0.2	29	5	Q33846	Microsatellite sequen	7.21e+01	219	18	0.2	40	29	T65725	Repeat sequence from	7.21e+01
147	18	0.2	30	5	Q33956	Microsatellite sequen	7.21e+01	220	19	0.2	40	5	Q33618	Repeat sequence from	7.21e+01
148	18	0.2	30	5	T65789	Repeat sequence from	7.21e+01	221	18	0.2	40	5	Q34091	Sequence of a microsa	1.97e+01
149	18	0.2	31	29	T65753	Repeat sequence from	7.21e+01	222	18	0.2	41	29	T65782	Repeat sequence from	7.21e+01
150	18	0.2	31	29	T65765	Repeat sequence from	7.21e+01	223	18	0.2	41	29	V33319	Anti-CD23 6G5 antibod	7.21e+01
151	18	0.2	31	29	T65759	Repeat sequence from	7.21e+01	224	18	0.2	41	29	T65758	Repeat sequence from	7.21e+01
152	18	0.2	31	5	Q34032	Microsatellite sequen	7.21e+01	225	18	0.2	41	29	T65745	Repeat sequence from	7.21e+01
153	18	0.2	31	5	Q33822	Microsatellite sequen	7.21e+01	226	18	0.2	41	29	T65783	Repeat sequence from	7.21e+01
154	18	0.2	31	5	Q33657	Microsatellite sequen	7.21e+01	227	19	0.2	41	29	T65710	Repeat sequence from	7.21e+01
155	18	0.2	31	5	Q34047	Microsatellite sequen	7.21e+01	228	18	0.2	41	5	Q33681	Microsatellite sequen	1.97e+01
											41	5	Q33801	Microsatellite sequen	7.21e+01

229	18	0.2	42 14	Q83950	Oligonucleotide clamp	7.21e+01	19	0.2	56 5	Q33548	Microsatellite sequen	1.97e+01
230	18	0.2	42 29	T65778	Repeat sequence from	7.21e+01	19	0.2	56 5	Q33603	Microsatellite sequen	1.97e+01
231	18	0.2	42 29	T65757	Repeat sequence from	7.21e+01	19	0.2	56 5	Q34056	Microsatellite sequen	1.97e+01
232	18	0.2	42 29	T65797	Repeat sequence from	7.21e+01	18	0.2	56 5	Q33813	Microsatellite sequen	7.21e+01
233	18	0.2	42 29	T65779	Repeat sequence from	7.21e+01	18	0.2	56 5	Q33654	Microsatellite sequen	7.21e+01
234	18	0.2	42 29	T65776	Repeat sequence from	7.21e+01	18	0.2	56 5	Q33947	Microsatellite sequen	7.21e+01
235	18	0.2	42 5	Q33770	Microsatellite sequen	7.21e+01	18	0.2	57 29	T65728	Repeat sequence from	7.21e+01
236	18	0.2	43 29	T65794	Repeat sequence from	7.21e+01	18	0.2	57 29	T65792	Repeat sequence from	7.21e+01
237	18	0.2	43 29	T65788	Repeat sequence from	7.21e+01	18	0.2	57 29	T65706	Repeat sequence from	7.21e+01
238	19	0.2	43 37	T97135	PCR primer used to am	1.97e+01	18	0.2	57 29	T65739	Repeat sequence from	7.21e+01
239	18	0.2	43 4	Q34006	Microsatellite sequen	7.21e+01	18	0.2	57 5	Q34100	Sequence of a microsa	7.21e+01
240	18	0.2	44 29	T65761	Repeat sequence from	7.21e+01	19	0.2	58 5	Q34116	Sequence of a microsa	1.97e+01
241	18	0.2	44 29	T65749	Repeat sequence from	7.21e+01	18	0.2	58 5	Q33858	Microsatellite sequen	7.21e+01
242	18	0.2	44 29	T65763	Repeat sequence from	7.21e+01	18	0.2	58 5	Q33755	Microsatellite sequen	7.21e+01
243	18	0.2	44 5	Q33636	Microsatellite sequen	7.21e+01	18	0.2	59 5	Q34173	Sequence of a microsa	7.21e+01
244	18	0.2	44 5	Q34104	Sequence of a microsa	7.21e+01	60 29	0.2	60 29	T65762	Repeat sequence from	1.97e+01
245	18	0.2	44 5	Q33983	Microsatellite sequen	7.21e+01	60 9	0.2	60 9	Q54430	(AC)30:(TG)30 polynuc	7.21e+01
246	18	0.2	44 5	Q34113	Sequence of a microsa	7.21e+01	60 36	0.2	60 36	T69881	Open circle probe #2	7.21e+01
247	19	0.2	45 29	T65737	Repeat sequence from	7.21e+01	60 5	0.2	60 5	Q33930	Microsatellite sequen	7.21e+01
248	18	0.2	45 29	T65751	Repeat sequence from	7.21e+01	60 5	0.2	60 5	Q33792	Microsatellite sequen	7.21e+01
249	18	0.2	45 29	T65786	Repeat sequence from	7.21e+01	61 29	0.2	61 29	T65766	Repeat sequence from	7.21e+01
250	19	0.2	45 5	Q34137	Sequence of a microsa	1.97e+01	61 5	0.2	61 5	Q34059	Microsatellite sequen	1.97e+01
251	18	0.2	45 5	Q33968	Microsatellite sequen	7.21e+01	62 29	0.2	62 29	T65704	Repeat sequence from	7.21e+01
252	18	0.2	45 5	Q33915	Microsatellite sequen	7.21e+01	62 5	0.2	62 5	Q33779	Microsatellite sequen	1.97e+01
253	19	0.2	46 29	T65709	Repeat sequence from	1.97e+01	62 1	0.2	62 1	Q03823	Poly GT enhancer elem	1.97e+01
254	18	0.2	46 56	V83640	Oligonucleotide 1 use	7.21e+01	63 5	0.2	63 5	Q33594	Microsatellite sequen	1.97e+01
255	18	0.2	46 29	T65756	Repeat sequence from	7.21e+01	63 5	0.2	63 5	Q33701	Microsatellite sequen	1.97e+01
256	18	0.2	46 29	T65719	Repeat sequence from	7.21e+01	63 5	0.2	63 5	Q33580	Microsatellite sequen	7.21e+01
257	18	0.2	46 5	Q33840	Microsatellite sequen	7.21e+01	64 5	0.2	64 5	Q33639	Microsatellite sequen	7.21e+01
258	18	0.2	46 56	V83641	Oligonucleotide 2 use	7.21e+01	65 29	0.2	65 29	T65724	Repeat sequence from	7.21e+01
259	18	0.2	46 5	Q33939	Microsatellite sequen	7.21e+01	65 29	0.2	65 29	T66072	(dC-dA)n.(dG-dT)n pol	7.21e+01
260	19	0.2	47 29	T66109	Microsatellite sequen	1.97e+01	65 29	0.2	65 29	T65730	Repeat sequence from	7.21e+01
261	18	0.2	47 29	T66060	(dC-dA)n.(dG-dT)n pol	7.21e+01	66 29	0.2	66 29	T65767	Repeat sequence from	7.21e+01
262	18	0.2	47 29	T65713	(dC-dA)n.(dG-dT)n pol	7.21e+01	68 5	0.2	68 5	Q34088	Sequence of a microsa	1.97e+01
263	18	0.2	47 56	V83636	Oligonucleotide 2 use	7.21e+01	70 5	0.2	70 5	Q34155	Sequence of a microsa	7.21e+01
264	18	0.2	47 29	T65716	Repeat sequence from	7.21e+01	72 29	0.2	72 29	T65729	Microsatellite sequen	7.21e+01
265	18	0.2	47 29	T65726	Repeat sequence from	7.21e+01	72 5	0.2	72 5	Q33600	Microsatellite sequen	7.21e+01
266	18	0.2	47 29	T65755	Repeat sequence from	7.21e+01	73 5	0.2	73 5	Q34140	Sequence of a microsa	1.97e+01
267	19	0.2	47 24	T30423	Compound in phase sim	1.97e+01	74 5	0.2	74 5	Q33651	Microsatellite sequen	7.21e+01
268	18	0.2	47 5	Q33834	Microsatellite sequen	7.21e+01	79 5	0.2	79 5	Q33936	Microsatellite sequen	1.97e+01
269	18	0.2	47 56	V83635	Oligonucleotide 1 use	7.21e+01	79 21	0.2	79 21	T25749	Human gene signature	7.21e+01
270	18	0.2	47 5	Q33959	Microsatellite sequen	7.21e+01	79 5	0.2	79 5	Q33795	Microsatellite sequen	7.21e+01
271	18	0.2	48 5	Q33798	Microsatellite sequen	7.21e+01	80 36	0.2	80 36	T69886	Open circle probe #3	7.21e+01
272	18	0.2	49 29	T65785	Repeat sequence from	7.21e+01	82 29	0.2	82 29	T65723	Repeat sequence from	7.21e+01
273	19	0.2	49 5	Q34122	Sequence of a microsa	1.97e+01	85 5	0.2	85 5	Q33624	Microsatellite sequen	7.21e+01
274	18	0.2	49 33	T80427	Hepatoma AS-30D Type	7.21e+01	86 5	0.2	86 5	Q34050	Microsatellite sequen	7.21e+01
275	19	0.2	50 29	T65791	Repeat sequence from	1.97e+01	89 29	0.2	89 29	T65718	Repeat sequence from	7.21e+01
276	18	0.2	50 14	Q83954	Oligonucleotide clamp	7.21e+01	91 29	0.2	91 29	T65740	Repeat sequence from	1.97e+01
277	18	0.2	50 29	T65774	Repeat sequence from	7.21e+01	91 29	0.2	91 29	T65721	Repeat sequence from	7.21e+01
278	18	0.2	50 29	T65717	Repeat sequence from	7.21e+01	92 29	0.2	92 29	T66081	(dC-dA)n.(dG-dT)n pol	1.97e+01
279	18	0.2	50 29	T65746	Repeat sequence from	7.21e+01	96 5	0.2	96 5	Q33526	Sequence of microsa	7.21e+01
280	18	0.2	50 29	T65787	Repeat sequence from	7.21e+01	98 5	0.2	98 5	Q33852	Microsatellite sequen	7.21e+01
281	18	0.2	50 29	T65741	Repeat sequence from	7.21e+01	109 29	0.2	109 29	T63496	Type 5 17-beta-hydrox	7.21e+01
282	18	0.2	50 4	Q34003	Microsatellite sequen	7.21e+01	110 13	0.2	110 13	Q79644	DNA region for primer	7.21e+01
283	18	0.2	51 29	T65771	Repeat sequence from	1.97e+01	112 44	0.2	112 44	V35669	Human genomic DNA tem	7.21e+01
284	18	0.2	51 29	T66075	(dC-dA)n.(dG-dT)n pol	7.21e+01	112 45	0.2	112 45	V39584	Mass spectrometric an	7.21e+01
285	18	0.2	51 29	T65777	Repeat sequence from	7.21e+01	114 5	0.2	114 5	Q34134	Sequence of a microsa	7.21e+01
286	18	0.2	51 29	T65795	Repeat sequence from	7.21e+01	135 44	0.2	135 44	V35671	Amplified DNA product	7.21e+01
287	18	0.2	51 29	T65764	Repeat sequence from	7.21e+01	135 45	0.2	135 45	V39586	Mass spectrometric an	7.21e+01
288	18	0.2	51 29	T65773	Repeat sequence from	7.21e+01	137 5	0.2	137 5	Q34062	Microsatellite marker	7.21e+01
289	18	0.2	51 29	T65715	Repeat sequence from	7.21e+01	141 19	0.2	141 19	T11256	Microsatellite marker	7.21e+01
290	19	0.2	51 5	Q34071	Microsatellite sequen	1.97e+01	141 22	0.2	141 22	T18871	Genotyping marker AFM	7.21e+01
291	18	0.2	52 29	T66069	(dC-dA)n.(dG-dT)n pol	7.21e+01	141 22	0.2	141 22	T28267	Survival motor neuron	1.97e+01
292	18	0.2	52 29	T66108	(dC-dA)n.(dG-dT)n pol	7.21e+01	142 36	0.2	142 36	T91730	Mouse SmlIM/CRP2 gene	7.21e+01
293	18	0.2	53 29	T65768	Repeat sequence from	7.21e+01	144 53	0.2	144 53	V89020	EST clone IK203	7.21e+01
294	19	0.2	54 5	Q33870	Microsatellite sequen	1.97e+01	149 43	0.2	149 43	V28929	Bovine Nramp1 generic	7.21e+01
295	18	0.2	54 11	Q45388	Oligonucleotide formi	7.21e+01	154 43	0.2	154 43	V28926	Bovine Nramp1 DNA SEQ	7.21e+01
296	18	0.2	55 5	Q33864	Microsatellite sequen	7.21e+01	155 29	0.2	155 29	T65670	Polymorphic repeat se	1.97e+01
297	19	0.2	56 29	T65735	Repeat sequence from	1.97e+01	155 43	0.2	155 43	V28927	Bovine Nramp1 generic	7.21e+01
298	19	0.2	56 29	T65707	Repeat sequence from	1.97e+01	155 43	0.2	155 43	V28923	Bovine Nramp1 DNA SEQ	7.21e+01
299	18	0.2	56 29	T66063	(dC-dA)n.(dG-dT)n pol	7.21e+01	160 40	0.2	160 40	V16145	Microsatellite marker	7.21e+01
300	18	0.2	56 29	T65769	Repeat sequence from	7.21e+01						
301	18	0.2	56 29	T65796	Repeat sequence from	7.21e+01						

375	18	0.2	165 43	V17750	Human breast cancer r	7.21e+01	18	0.2	293 29	T65700	Polymorphic repeat se	7.21e+01
376	18	0.2	175 29	T65655	Polymorphic repeat se	7.21e+01	18	0.2	294 52	V68893	DNA molecule encoding	7.21e+01
377	19	0.2	177 11	Q77282	Human genome fragment	1.97e+01	18	0.2	294 19	T11255	Microsatellite marker	7.21e+01
378	18	0.2	178 29	T65662	Polymorphic repeat se	7.21e+01	18	0.2	294 22	T28266	Survival motor neuron	7.21e+01
379	19	0.2	179 29	T65677	Polymorphic repeat se	7.21e+01	18	0.2	294 22	T18870	Genotyping marker C27	7.21e+01
380	18	0.2	180 29	T65657	Polymorphic repeat se	7.21e+01	18	0.2	296 30	T43933	Sequence flanking mar	7.21e+01
381	18	0.2	183 29	T65671	Polymorphic repeat se	7.21e+01	18	0.2	296 30	T72053	Sequence flanking mar	7.21e+01
382	18	0.2	186 29	T65663	Polymorphic repeat se	7.21e+01	18	0.2	297 29	T65684	Polymorphic repeat se	7.21e+01
383	18	0.2	190 29	T65664	Polymorphic repeat se	7.21e+01	18	0.2	298 30	T43934	Sequence flanking mar	7.21e+01
384	19	0.2	191 29	T65672	Polymorphic repeat se	7.21e+01	18	0.2	298 30	T72054	Sequence flanking mar	7.21e+01
385	19	0.2	192 19	T20350	Human gene signature	1.97e+01	18	0.2	299 54	V87891	EST clone FG340.	7.21e+01
386	18	0.2	194 3	Q20374	Sequence of a human (7.21e+01	19	0.2	300 29	T65696	Polymorphic repeat se	1.97e+01
387	18	0.2	194 29	T65666	Polymorphic repeat se	7.21e+01	19	0.2	300 49	V48143	Z-chromosomal microsa	1.97e+01
388	18	0.2	194 49	V48139	Z-chromosomal microsa	7.21e+01	19	0.2	301 53	V90480	EST clone DT719.	1.97e+01
389	19	0.2	197 3	Q15206	Phage phi2-22 subclon	1.97e+01	18	0.2	305 19	T11257	Microsatellite marker	7.21e+01
390	18	0.2	198 29	T65693	Polymorphic repeat se	7.21e+01	18	0.2	305 22	T18872	Genotyping marker C16	7.21e+01
391	18	0.2	198 49	V48138	Polymorphic repeat se	7.21e+01	18	0.2	305 22	T28268	Survival motor neuron	7.21e+01
392	18	0.2	200 22	T26777	Z-chromosomal microsa	7.21e+01	18	0.2	305 8	Q59406	Human brain Expressed	7.21e+01
393	18	0.2	200 49	V48140	Human gene signature	7.21e+01	18	0.2	315 60	X13780	Enterococcus faecalis	7.21e+01
394	18	0.2	200 29	T65659	Polymorphic repeat se	7.21e+01	18	0.2	317 53	V89470	EST clone CO244.	7.21e+01
395	18	0.2	202 29	T65689	Polymorphic repeat se	7.21e+01	19	0.2	318 29	T65653	Polymorphic repeat se	1.97e+01
396	18	0.2	203 29	T65658	Polymorphic repeat se	7.21e+01	18	0.2	319 53	V90110	EST clone DG329.	7.21e+01
397	19	0.2	208 29	T65692	Polymorphic repeat se	1.97e+01	18	0.2	323 29	T65682	Polymorphic repeat se	7.21e+01
398	19	0.2	210 29	T65674	Polymorphic repeat se	1.97e+01	19	0.2	324 29	T65687	Polymorphic repeat se	1.97e+01
399	19	0.2	211 29	T65673	Polymorphic repeat se	1.97e+01	19	0.2	332 10	Q56704	Sequence of the CACAC	1.97e+01
400	19	0.2	214 29	T65688	Polymorphic repeat se	1.97e+01	19	0.2	332 18	T19130	Human gene signature	7.21e+01
401	18	0.2	218 40	V09101	5' nucleotide sequenc	7.21e+01	18	0.2	332 18	T19130	Human gene signature	7.21e+01
402	18	0.2	218 41	V15715	Clone CC397_19 5'	7.21e+01	18	0.2	338 8	Q60357	Human brain Expressed	7.21e+01
403	18	0.2	219 4	Q27094	Fragile X diagnostic	7.21e+01	18	0.2	340 30	T43951	Sequence flanking mar	7.21e+01
404	18	0.2	221 11	Q77331	Human genome fragment	7.21e+01	18	0.2	345 29	T65686	Polymorphic repeat se	7.21e+01
405	18	0.2	221 29	T65668	Polymorphic repeat se	7.21e+01	18	0.2	348 23	T26180	Human gene signature	7.21e+01
406	19	0.2	223 29	T65665	Polymorphic repeat se	1.97e+01	18	0.2	350 22	T28269	Survival motor neuron	7.21e+01
407	18	0.2	224 6	Q36138	Bovine male specific	7.21e+01	18	0.2	350 22	T18873	Genotyping marker C17	7.21e+01
408	18	0.2	225 43	V17749	Human breast cancer r	7.21e+01	18	0.2	350 19	T11258	Microsatellite marker	7.21e+01
409	18	0.2	225 29	T65678	Polymorphic repeat se	7.21e+01	19	0.2	353 8	Q61364	Human brain Expressed	1.97e+01
410	18	0.2	226 19	T21161	Human gene signature	7.21e+01	19	0.2	355 49	V48131	Z-chromosomal microsa	1.97e+01
411	19	0.2	228 29	T65694	Polymorphic repeat se	1.97e+01	18	0.2	363 30	T72066	Sequence flanking mar	7.21e+01
412	19	0.2	230 29	T65667	Polymorphic repeat se	1.97e+01	18	0.2	363 30	T43946	Sequence flanking mar	7.21e+01
413	18	0.2	231 19	T22702	Human gene signature	7.21e+01	18	0.2	365 29	T65685	Polymorphic repeat se	7.21e+01
414	19	0.2	235 21	T24383	Human gene signature	7.21e+01	18	0.2	372 19	T11254	Microsatellite marker	7.21e+01
415	18	0.2	236 29	T65701	Polymorphic repeat se	1.97e+01	18	0.2	372 22	T28265	Survival motor neuron	7.21e+01
416	19	0.2	236 30	T72065	Sequence flanking mar	1.97e+01	18	0.2	372 22	T18869	Genotyping marker C21	7.21e+01
417	19	0.2	236 30	T43945	Sequence flanking mar	1.97e+01	19	0.2	372 10	Q55242	Gravine ribosomal c	1.97e+01
418	18	0.2	240 29	T65676	Polymorphic repeat se	7.21e+01	19	0.2	376 10	Q55247	Gravine ribosomal c	1.97e+01
419	18	0.2	240 29	T65681	Polymorphic repeat se	7.21e+01	18	0.2	378 54	V87853	EST clone FB78.	7.21e+01
420	18	0.2	240 29	T65660	Polymorphic repeat se	7.21e+01	18	0.2	379 19	T21354	Human gene signature	7.21e+01
421	18	0.2	242 29	T65654	Polymorphic repeat se	7.21e+01	18	0.2	380 30	T43953	Sequence flanking mar	7.21e+01
422	18	0.2	243 29	T65691	Polymorphic repeat se	7.21e+01	19	0.2	382 10	Q55246	Gravine ribosomal c	1.97e+01
423	19	0.2	244 29	T65680	Polymorphic repeat se	7.21e+01	18	0.2	385 30	T43955	Sequence flanking mar	7.21e+01
424	18	0.2	244 29	T65699	Polymorphic repeat se	1.97e+01	18	0.2	387 29	T65695	Polymorphic repeat se	7.21e+01
425	19	0.2	245 44	V30918	Polymorphic repeat se	7.21e+01	18	0.2	389 53	V90181	EST clone DGL21.	7.21e+01
426	18	0.2	249 29	T65679	Human secreted protei	1.97e+01	18	0.2	394 8	Q61181	Human brain Expressed	7.21e+01
427	19	0.2	250 10	Q55248	Gravine ribosomal c	7.21e+01	18	0.2	395 49	V48141	Z-chromosomal microsa	7.21e+01
428	19	0.2	258 5	Q32866	Probe VAW409 for diag	1.97e+01	19	0.2	406 52	V69000	DNA molecule encoding	1.97e+01
429	18	0.2	258 53	V89477	EST clone CO204.	7.21e+01	18	0.2	412 42	V29337	Calcium ion channel a	7.21e+01
430	18	0.2	259 29	T65675	Polymorphic repeat se	7.21e+01	19	0.2	414 24	T38262	105 gene differential	7.21e+01
431	18	0.2	259 29	T65698	Polymorphic repeat se	7.21e+01	19	0.2	415 8	Q59296	Human brain Expressed	1.97e+01
432	18	0.2	261 29	T65656	Polymorphic repeat se	7.21e+01	19	0.2	415 6	Q39884	Expressed Sequence Ta	1.97e+01
433	18	0.2	262 29	T65697	Polymorphic repeat se	7.21e+01	18	0.2	422 49	V48135	Z-chromosomal microsa	7.21e+01
434	18	0.2	264 29	T65661	Polymorphic repeat se	7.21e+01	18	0.2	429 54	V87719	EST clone EJ280.	7.21e+01
435	18	0.2	264 29	T65690	Polymorphic repeat se	7.21e+01	18	0.2	429 30	T43952	Sequence flanking mar	7.21e+01
436	18	0.2	265 29	T65652	Polymorphic repeat se	7.21e+01	18	0.2	434 42	V23146	3' fragment of Rat Pu	7.21e+01
437	18	0.2	266 53	V88979	EST clone IJ1201.	7.21e+01	18	0.2	447 49	V48142	Z-chromosomal microsa	7.21e+01
438	18	0.2	266 4	Q27097	Fragile X diagnostic	7.21e+01	18	0.2	448 35	T68682	Penaeus vannamei geno	7.21e+01
439	18	0.2	268 20	T21902	Human gene signature	7.21e+01	19	0.2	469 33	T80579	Human plasma platelet	1.97e+01
440	18	0.2	270 29	T65702	Polymorphic repeat se	7.21e+01	19	0.2	469 34	T87063	Human platelet-activa	1.97e+01
441	19	0.2	274 8	Q60455	Human brain Expressed	1.97e+01	19	0.2	469 15	Q87964	Human acetyl hydrolas	1.97e+01
442	18	0.2	278 29	V65703	Polymorphic repeat se	7.21e+01	19	0.2	469 37	T96146	Human plasma platelet	1.97e+01
443	19	0.2	280 49	V48136	Polymorphic repeat se	7.21e+01	19	0.2	469 53	V08549	Human PAF-AH coding s	1.97e+01
444	18	0.2	282 4	Q27100	Z-chromosomal microsa	1.97e+01	19	0.2	469 29	T66136	PAF-AH exon 12 and pa	1.97e+01
445	18	0.2	283 8	Q60960	Fragile X diagnostic	7.21e+01	18	0.2	477 51	V61236	cdNA sequence of pros	7.21e+01
446	19	0.2	285 49	V48130	Human brain Expressed	7.21e+01	18	0.2	477 49	V58621	Prostate tumour speci	7.21e+01
447	18	0.2	289 49	V48145	Z-chromosomal microsa	7.21e+01	19	0.2	478 49	V48137	Z-chromosomal microsa	7.21e+01
									489 30	T43939	Sequence flanking mar	1.97e+01

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521	19	0.2	489 30	T72059	Sequence flanking mar	1.97e+01	18	594	0.2	1275 56	V84529	Human secreted protei	7.21e+01
522	18	0.2	500 60	X13700	Enterococcus faecalis	7.21e+01	18	595	0.2	1302 24	T43045	Helicobacter pylori p	7.21e+01
523	19	0.2	502 7	V46914	Human Kunitz-type pro	1.97e+01	18	596	0.2	1307 56	V84569	Human secreted protei	7.21e+01
524	18	0.2	508 53	Q69714	3' portion of intron	7.21e+01	18	597	0.2	1325 42	V20808	Mus musculus vascular	7.21e+01
525	18	0.2	537 60	X13917	Enterococcus faecalis	7.21e+01	18	598	0.2	1329 50	V33199	Secreted protein FB78	7.21e+01
526	19	0.2	543 16	Q85537	DNA probe 43 detects	1.97e+01	18	599	0.2	1371 52	V33199	Mouse neutrophil elas	7.21e+01
527	19	0.2	545 30	T43932	Sequence flanking mar	1.97e+01	19	600	0.2	1400 12	Q70142	Human cartilage link	1.97e+01
528	19	0.2	545 30	T72052	Sequence flanking mar	1.97e+01	19	601	0.2	1427 41	V09663	Human cathepsin K gen	1.97e+01
529	18	0.2	557 38	V06158	Tumour suppression ge	7.21e+01	19	602	0.2	1429 17	T05625	Neurotrophin-6 cDNA	1.97e+01
530	19	0.2	560 2	N60553	Fragment of plasmid p	1.97e+01	19	603	0.2	1442 19	Q98919	TGF-beta inducible re	1.97e+01
531	19	0.2	560 1	Q06235	Bovine male-specific	1.97e+01	19	604	0.2	1470 30	T72063	Sequence flanking mar	1.97e+01
532	18	0.2	571 28	T33598	Mouse fibrosin cDNA	7.21e+01	19	605	0.2	1470 30	T43943	Sequence flanking mar	1.97e+01
533	18	0.2	571 28	T61383	Mouse fibrosin cDNA	7.21e+01	19	606	0.2	1493 5	Q28411	Glia activating facto	7.21e+01
534	19	0.2	585 43	V28925	Bison Nramp1 DNA SEQ	1.97e+01	18	607	0.2	1517 51	V59788	Human secreted protei	7.21e+01
535	19	0.2	587 43	V28928	Bison Nramp1 DNA SEQ	1.97e+01	18	608	0.2	1528 26	T45972	Mouse utrophin gene p	7.21e+01
536	19	0.2	592 16	Q85520	DNA probe 26 detects	1.97e+01	18	609	0.2	1533 30	T71575	Exon 1 of LETO rat ch	7.21e+01
537	18	0.2	594 53	V88419	EST clone EK634	7.21e+01	18	610	0.2	1538 3	Q21732	DNA encoding a RAP-2	7.21e+01
538	18	0.2	597 16	Q92942	Natural resistance-as	7.21e+01	18	611	0.2	1542 25	T42305	Male-specific DNA seq	7.21e+01
539	19	0.2	600 30	T43950	Sequence flanking mar	1.97e+01	18	612	0.2	1548 1	N80038	Colony stimulating ge	7.21e+01
540	18	0.2	605 30	T72055	Sequence flanking mar	7.21e+01	18	613	0.2	1549 1	N80398	Region upstream of co	7.21e+01
541	18	0.2	605 30	T43935	Sequence flanking mar	7.21e+01	18	614	0.2	1557 50	V46430	Mouse osteocalcin B g	7.21e+01
542	18	0.2	637 22	T18874	Human survival motor	7.21e+01	19	615	0.2	1560 37	T88012	Murine CD3delta T cel	1.97e+01
543	18	0.2	672 30	T43948	Sequence flanking mar	7.21e+01	19	616	0.2	1560 37	T88012	Murine CD3delta T cel	1.97e+01
544	18	0.2	688 30	T72060	Sequence flanking mar	7.21e+01	19	617	0.2	1570 17	T01048	Mouse B7-1 exons 1, 3	1.97e+01
545	18	0.2	688 30	T43940	Sequence flanking mar	7.21e+01	19	618	0.2	1577 5	Q31726	Rat IgH 3'-enhancer	1.97e+01
546	19	0.2	698 38	V06140	Viral infection gene	1.97e+01	18	619	0.2	1579 47	V41689	Nucleotide sequence o	7.21e+01
547	18	0.2	704 49	V61632	Human TACE-like DNA	7.21e+01	18	620	0.2	1586 40	V15213	Human osteogenic fusi	7.21e+01
548	19	0.2	705 30	T72057	Sequence flanking mar	1.97e+01	18	621	0.2	1586 60	X00238	Osteogenic fusion pro	7.21e+01
549	19	0.2	705 30	T43937	Sequence flanking mar	1.97e+01	18	622	0.2	1586 9	Q53150	Sequence encoding ost	7.21e+01
550	19	0.2	724 30	T72064	Sequence flanking mar	1.97e+01	18	623	0.2	1586 18	T02610	CBMP2b2 cDNA encoding	7.21e+01
551	19	0.2	724 30	T43944	Sequence flanking mar	1.97e+01	18	624	0.2	1606 17	T01050	Mouse B7-1 exons 1, 2	1.97e+01
552	18	0.2	751 30	T43931	Sequence flanking mar	1.97e+01	19	625	0.2	1614 24	T40206	Tobacco lycopene cycl	7.21e+01
553	18	0.2	751 30	T72051	Sequence flanking mar	7.21e+01	18	626	0.2	1647 9	Q52272	Human RADcompB cDNA s	7.21e+01
554	19	0.2	761 19	Q98920	Sequence flanking mar	7.21e+01	18	627	0.2	1647 35	T91036	Human checkpoint gene	7.21e+01
555	19	0.2	766 52	V65399	TGF-beta inducible re	1.97e+01	18	628	0.2	1686 7	Q43957	Bone morphogenetic pr	7.21e+01
556	18	0.2	780 30	T43181	Promoter sequence of	1.97e+01	18	629	0.2	1690 60	V70894	CDNA encoding human Z	7.21e+01
557	19	0.2	818 17	T01034	5'ALT DNA sequence co	7.21e+01	19	630	0.2	1700 2	Q12032	Gastrin releasing pep	1.97e+01
558	18	0.2	829 42	V29366	Mouse B7-1 exon 6 (Cy	1.97e+01	19	631	0.2	1700 2	Q11844	Encodes gastrin relea	1.97e+01
559	18	0.2	835 38	V06122	Calcium ion channel a	7.21e+01	19	632	0.2	1700 5	Q29158	Mouse R1BP (GRP-R)	1.97e+01
560	19	0.2	848 2	Q13632	Viral infection gene	7.21e+01	18	633	0.2	1732 52	V34305	Human secreted protei	7.21e+01
561	18	0.2	867 35	T66791	GBMT modified transcr	1.97e+01	18	634	0.2	1758 48	V44597	Mouse uncoupling prot	7.21e+01
562	18	0.2	875 49	V58364	Partial seq. obtained	7.21e+01	18	635	0.2	1788 60	X00232	Human osteogenic prot	7.21e+01
563	18	0.2	882 22	T14630	Coding sequence for s	7.21e+01	18	636	0.2	1788 12	Q72710	Prepro human CBMP2B c	7.21e+01
564	18	0.2	884 38	V06156	Tie receptor tyrosine	7.21e+01	18	637	0.2	1788 18	T02601	Human CBMP2(b) cDNA	7.21e+01
565	18	0.2	970 55	V08841	Tumour suppression ge	7.21e+01	18	638	0.2	1788 9	Q53144	Sequence encoding ost	7.21e+01
566	18	0.2	972 30	T68932	Gene No. 31 encoding	7.21e+01	18	639	0.2	1788 40	V15207	Human osteogenic prot	7.21e+01
567	18	0.2	1000 30	T72062	Bovine PIR-1 exon 6 s	7.21e+01	18	640	0.2	1790 50	V53207	Human Fas ligand cDNA	7.21e+01
568	18	0.2	1000 30	T43942	Sequence flanking mar	7.21e+01	18	641	0.2	1790 49	V32994	Fas Ligand cDNA	7.21e+01
569	19	0.2	1016 12	Q70049	Sequence flanking mar	1.97e+01	18	642	0.2	1813 60	V70895	CDNA encoding an alle	7.21e+01
570	19	0.2	1045 30	T43938	Dirofilaria immitis p	1.97e+01	18	643	0.2	1841 15	Q91311	Human Fas-L gene	7.21e+01
571	19	0.2	1045 30	T72058	Sequence flanking mar	1.97e+01	18	644	0.2	1851 28	T42097	Portion of mouse geno	7.21e+01
572	19	0.2	1050 30	T43927	Sequence flanking mar	7.21e+01	19	645	0.2	1867 32	T80385	DNA encoding LmeIF4A	1.97e+01
573	18	0.2	1050 30	T72047	Sequence around marke	7.21e+01	19	646	0.2	1876 12	Q71053	Rabbit C7-alpha-H cor	1.97e+01
574	18	0.2	1091 60	X13502	Sequence around marke	7.21e+01	18	647	0.2	1876 28	T29743	Mouse inositol polyph	7.21e+01
575	18	0.2	1139 1	N90255	Enterococcus faecalis	7.21e+01	19	648	0.2	1888 17	T01039	Mouse B7-1 exons 1, 2	1.97e+01
576	18	0.2	1139 1	N80299	Interleukin-6	7.21e+01	18	649	0.2	1890 45	V39009	Nucleotide sequence o	7.21e+01
577	18	0.2	1166 30	T43941	Interleukin 6	7.21e+01	18	650	0.2	1905 23	T29986	Human Fas ligand gene	7.21e+01
578	18	0.2	1166 30	T72061	Sequence flanking mar	7.21e+01	18	651	0.2	1906 51	V59637	Human secreted protei	7.21e+01
579	19	0.2	1176 2	Q10063	Sequence flanking mar	1.97e+01	19	652	0.2	1921 32	T58786	CDNA encoding C-CAM1	1.97e+01
580	18	0.2	1194 2	N70395	Bovine Y-specific seq	7.21e+01	18	653	0.2	1921 1	N90612	CD19 cDNA	7.21e+01
581	19	0.2	1199 6	Q36051	Sequence encoding rat	7.21e+01	18	654	0.2	1922 3	Q21172	Human CD19 antigen co	7.21e+01
582	18	0.2	1215 28	T58339	Human nov gene promot	1.97e+01	18	655	0.2	1922 24	T38556	Human CD19 antigen cD	7.21e+01
583	19	0.2	1217 3	N40211	Tobacco epi-5-aristol	1.97e+01	18	656	0.2	1922 22	T14712	Homo sapiens clone BG	7.21e+01
584	18	0.2	1231 38	T95755	DNA sequence encoding	7.21e+01	18	657	0.2	1939 46	V32415	Stress activated prot	7.21e+01
585	18	0.2	1245 7	Q41102	Arabidopsis SCARECROW	7.21e+01	18	658	0.2	1975 17	T10640	Stress activated prot	7.21e+01
586	18	0.2	1245 44	V35607	HME1	7.21e+01	18	659	0.2	1986 17	T10641	Sequence of the chole	7.21e+01
587	18	0.2	1249 1	Q06091	Human mammary epithel	7.21e+01	18	660	0.2	2015 8	Q47670	Sequence of the chole	7.21e+01
588	18	0.2	1249 1	Q06091	Murine cellular enhan	7.21e+01	18	661	0.2	2027 47	V07477	Human protease nexin	7.21e+01
589	18	0.2	1257 2	N70394	Murine cellular enhan	7.21e+01	18	662	0.2	2028 15	Q89924	Protease Nexin-1 type	7.21e+01
590	18	0.2	1260 30	T72049	Sequence encoding hum	7.21e+01	18	663	0.2	2028 47	V07476	Human protease nexin	7.21e+01
591	18	0.2	1260 30	T43929	Sequence around marke	7.21e+01	18	664	0.2	2029 3	Q20496	PN-I alpha analogue	7.21e+01
592	18	0.2	1260 30	T72045	Sequence around marke	7.21e+01	18	665	0.2	2029 3	Q20494	PN-I alpha analogue	7.21e+01
593	18	0.2	1260 30	T43925	Sequence around marke	7.21e+01	18	666	0.2	2029 1	N81281	Sequence of coding re	7.21e+01

C	667	18	0.2	2029	3	Q20495	PN-I alpha analogue, Protease Nexin-1 type	7.21e+01	C	740	19	0.2	2703	29	T59729	Human bone morphogeni cDNA for human MP52.	1.97e+01
C	668	18	0.2	2031	15	Q89925	Sequence of coding re	7.21e+01	C	741	19	0.2	2703	38	T98191	CDNA encoding human p	1.97e+01
C	669	18	0.2	2031	1	N81282	PN-I beta analogue, p	7.21e+01	C	742	19	0.2	2703	33	T61412	DNA encoding human TG	1.97e+01
C	670	18	0.2	2032	3	Q22587	PN-I beta analogue, p	7.21e+01	C	743	19	0.2	2703	36	T69695	Human MP52 cDNA.	1.97e+01
C	671	18	0.2	2032	3	Q22586	PN-I beta analogue, p	7.21e+01	C	744	19	0.2	2703	39	T88340	DNA encoding human MP	1.97e+01
C	672	18	0.2	2032	3	Q22585	Human secreted protei	1.97e+01	C	745	19	0.2	2703	32	T59405	200 gene differential	1.97e+01
C	673	19	0.2	2033	52	V34207	Mouse SNAP-25 polypep	7.21e+01	C	746	19	0.2	2712	24	T38265	Murine C140 receptor	7.21e+01
C	674	18	0.2	2040	50	V57558	Mouse synaptosomal-as	7.21e+01	C	747	18	0.2	2732	14	Q84559	Rabbit protein-couple	7.21e+01
C	675	18	0.2	2040	38	V01554	Sequence flanking mar	7.21e+01	C	748	18	0.2	2732	27	T32038	Barley alpha-glucosid	1.97e+01
C	676	18	0.2	2040	30	T43949	Human metalloproteina	7.21e+01	C	749	18	0.2	2746	55	V72893	Sequence flanking mar	1.97e+01
C	677	18	0.2	2057	29	T63123	Human connective tiss	7.21e+01	C	750	19	0.2	2752	43	V11736	Sequence flanking mar	1.97e+01
C	678	18	0.2	2075	28	T45360	Human connective tiss	7.21e+01	C	751	19	0.2	2757	30	T43936	G-protein coupled rec	1.97e+01
C	679	18	0.2	2075	44	V38085	Human connective tiss	7.21e+01	C	752	19	0.2	2757	30	T72056	Rat androgen receptor	7.21e+01
C	680	18	0.2	2075	18	T04226	Connective tissue gro	7.21e+01	C	753	18	0.2	2764	31	T43351	Chick p75 cDNA.	7.21e+01
C	681	18	0.2	2075	26	T51234	Connective tissue gro	7.21e+01	C	754	18	0.2	2775	25	T47511	Killer cell activator	7.21e+01
C	682	18	0.2	2085	44	V32028	Nucleotide sequence o	7.21e+01	C	755	18	0.2	2783	15	Q92367	Killer cell activator	7.21e+01
C	683	18	0.2	2099	47	V51370	Human TIGR exon 3 DNA	7.21e+01	C	756	18	0.2	2838	57	V83507	Unique 2.9 kb genomic	7.21e+01
C	684	18	0.2	2107	33	T86264	Rat brain Neuroglycan	7.21e+01	C	757	18	0.2	2838	57	V83507	Human cytokine respon	7.21e+01
C	685	18	0.2	2110	7	Q41228	Clone GP22 encoding m	7.21e+01	C	758	18	0.2	2858	13	Q75270	Delta cDNA D11.	7.21e+01
C	686	18	0.2	2116	46	V32619	Mouse preprotachykin	7.21e+01	C	759	18	0.2	2866	27	T43383	Murine hyaluronan syn	1.97e+01
C	687	19	0.2	2136	52	V34263	Human secreted protei	1.97e+01	C	760	18	0.2	2892	5	Q30997	Full length cytochrom	1.97e+01
C	688	19	0.2	2160	11	Q66641	Mouse Activin recepto	7.21e+01	C	761	19	0.2	2919	30	T51124	Histamine H1 receptor	1.97e+01
C	689	18	0.2	2182	3	Q08510	Apoptosis-regulating	7.21e+01	C	762	19	0.2	2947	40	V18821	Natural resistance-as	7.21e+01
C	690	18	0.2	2186	50	V57441	Sequence of amylase g	7.21e+01	C	763	19	0.2	2956	37	T99140	Rat glucagon-like pep	7.21e+01
C	691	18	0.2	2215	60	V99330	Human tumour necrosis	1.97e+01	C	764	19	0.2	2960	7	Q42561	Rat opiod receptor g	7.21e+01
C	692	19	0.2	2220	14	Q84048	CDNA encoding a GDNFR	7.21e+01	C	765	18	0.2	2967	15	Q87171	Genomic sequence enco	7.21e+01
C	693	18	0.2	2220	10	Q84048	Insertion sequence PH	7.21e+01	C	766	18	0.2	2972	20	T03574	Sequence encoding pro	1.97e+01
C	694	18	0.2	2240	36	T30773	CD40 associated prote	7.21e+01	C	767	19	0.2	2995	57	V64417	Human t-complex assoc	7.21e+01
C	695	18	0.2	2263	57	V80628	Kidney injury associa	7.21e+01	C	768	19	0.2	2997	17	T11641	Leishmania antigen M1	7.21e+01
C	696	18	0.2	2271	43	V28936	Bovine Nramp1 encodin	7.21e+01	C	769	19	0.2	3000	38	V01547	Deleted in polyposi	7.21e+01
C	697	18	0.2	2298	47	V42548	Mouse dectin-1 cDNA.	1.97e+01	C	770	19	0.2	3025	6	Q39966	Human TB2 gene.	7.21e+01
C	698	19	0.2	2299	17	T11640	Murine osteogenic pro	7.21e+01	C	771	18	0.2	3046	44	V29074	Human TB2 cDNA.	7.21e+01
C	699	18	0.2	2308	6	Q35148	Rat DLB dopamine rece	1.97e+01	C	772	18	0.2	3048	40	V15294	Encodes DPL gene in f	7.21e+01
C	700	18	0.2	2310	29	T47712	Mouse bone morphogene	7.21e+01	C	773	18	0.2	3054	7	Q42406	CD22-beta gene.	7.21e+01
C	701	18	0.2	2312	2	Q12020	Sequence of Wilm's tu	7.21e+01	C	774	18	0.2	3066	8	Q48985	Human hepatoma-derive	1.97e+01
C	702	18	0.2	2312	40	V17060	Wilms' tumour polypep	7.21e+01	C	775	18	0.2	3069	9	Q51015	Human fsh15w6 gene.	1.97e+01
C	703	18	0.2	2315	52	V34322	Human secreted protei	7.21e+01	C	776	18	0.2	3096	2	N71063	DNA encoding a Staphy	7.21e+01
C	704	18	0.2	2319	52	V64070	Arabidopsis thaliana	7.21e+01	C	777	19	0.2	3114	1	N80336	Inulinase coding sequ	7.21e+01
C	705	18	0.2	2334	39	V09695	M. hyopneumoniae 2.3k	1.97e+01	C	778	18	0.2	3120	7	Q39261	CDNA encoding avenaci	7.21e+01
C	706	19	0.2	2338	2	Q13575	DHR3 gene.	1.97e+01	C	779	18	0.2	3120	7	Q39261	Mouse intereukin-17	7.21e+01
C	707	19	0.2	2349	57	V80608	Kidney injury associa	1.97e+01	C	780	18	0.2	3134	30	T62135	Clone AQ73_3 coding s	1.97e+01
C	708	18	0.2	2352	30	T63604	Dehiscence zone-selec	7.21e+01	C	781	18	0.2	3134	48	V47555	Rat neurtrurin recepto	7.21e+01
C	709	18	0.2	2359	22	T31273	LMPI associated prote	7.21e+01	C	782	18	0.2	3171	12	Q72332	Sequence encoding new	7.21e+01
C	710	18	0.2	2396	53	V69703	3' UTR sequence of ie	7.21e+01	C	783	18	0.2	3172	37	T96154	Human TB2 gene.	7.21e+01
C	711	18	0.2	2403	36	T97870	CDNA encoding a chime	7.21e+01	C	784	18	0.2	3172	36	T95539	Human TB2 cDNA.	7.21e+01
C	712	18	0.2	2412	36	T97869	CDNA encoding a chime	7.21e+01	C	785	18	0.2	3172	49	V56448	Encodes DPL gene in f	7.21e+01
C	713	18	0.2	2433	23	T29396	Apoptosis participati	7.21e+01	C	786	18	0.2	3172	4	Q27235	CD22-beta gene.	7.21e+01
C	714	18	0.2	2436	51	V59776	Human secreted protei	7.21e+01	C	787	18	0.2	3190	6	Q38746	Human hepatoma-derive	1.97e+01
C	715	19	0.2	2446	17	T08768	Rat biglycan cDNA.	1.97e+01	C	788	19	0.2	3202	29	T47520	Human fsh15w6 gene.	1.97e+01
C	716	18	0.2	2456	22	T33278	Human intereukin-11	7.21e+01	C	789	19	0.2	3216	51	V33493	DNA encoding a Staphy	7.21e+01
C	717	18	0.2	2458	17	T16306	Arabidopsis HY4 cDNA	7.21e+01	C	790	18	0.2	3222	43	T84011	Inulinase coding sequ	1.97e+01
C	718	18	0.2	2460	30	T67106	Murine lymphoid enhan	7.21e+01	C	791	19	0.2	3223	11	Q66475	CDNA encoding avenaci	7.21e+01
C	719	18	0.2	2463	3	Q20810	EcoRI fragment encodi	7.21e+01	C	792	18	0.2	3269	17	T06024	Mouse intereukin-17	7.21e+01
C	720	19	0.2	2483	30	T45982	Human cocaine and amp	1.97e+01									

813	18	0.2	3573	1	N81065	Sequence of human thr	7.21e+01	18	886	5150	33	T78598	AS-30D tumour Type II	7.21e+01
814	19	0.2	3582	50	V62430	Prostate cancer antig	1.97e+01	18	887	5153	21	T30347	Human YAP cDNA.	7.21e+01
815	18	0.2	3588	2	N70317	Sequence encoding por	7.21e+01	18	888	5232	48	V55038	Human XIAP coding seq	7.21e+01
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817	18	0.2	3640	1	N82026	Cloned p2.1 insert en	7.21e+01	18	890	5240	50	V48268	P. chrysogenum beta-N	7.21e+01
818	18	0.2	3678	56	V72671	Hamster EF-1 alpha tr	7.21e+01	18	891	5299	47	V51361	Human TIGR promoter r	7.21e+01
819	18	0.2	3680	22	T33559	Leukemia inhibiting	7.21e+01	18	892	5300	47	V51366	Human TIGR promoter m	7.21e+01
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823	19	0.2	3699	28	T37237	Heavy chain minilocus	1.97e+01	18	896	5300	47	V51365	Human TIGR promoter m	7.21e+01
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828	18	0.2	3727	42	V11126	Rat SH2 binding prote	7.21e+01	18	901	5631	24	T08803	Polycystic kidney dis	7.21e+01
829	18	0.2	3751	11	Q62461	Human embryonal kinas	7.21e+01	18	902	5720	25	T42117	Lats gene encoding la	7.21e+01
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831	18	0.2	3757	47	V42708	Mouse mast cell prote	7.21e+01	18	904	5961	16	Q74060	Human interferon-gamm	1.97e+01
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835	18	0.2	3812	2	Q10991	Partial sequence of m	7.21e+01	18	908	6259	38	T86366	SM22 protein gene nuc	7.21e+01
836	18	0.2	3821	9	Q56609	Human PGF-2/NT-3 5' f	7.21e+01	18	909	6305	16	Q96127	Tobacco leaf antifung	7.21e+01
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838	18	0.2	3831	3	Q20262	ERK3.	7.21e+01	18	911	6418	10	Q65395	Osteogenic protein ho	7.21e+01
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847	19	0.2	4091	1	Q04035	Stem cell leukaemia (1.97e+01	18	920	7623	36	T60556	Plasmid pAdneo-int us	1.97e+01
848	19	0.2	4102	36	T85575	Human WSX receptor va	1.97e+01	19	921	7920	20	T05899	Human IL-4 gene.	1.97e+01
849	18	0.2	4118	25	T44520	NTHI hxc + hxb gene	7.21e+01	19	922	7997	34	T79737	Rat cholesterol 7-alp	1.97e+01
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853	18	0.2	4157	40	V19709	5-aminolevulinic acid	7.21e+01	18	926	8045	17	T12237	Retroviral vector MFG	7.21e+01
854	18	0.2	4157	40	V04102	Aspergillus oryzae 5-	7.21e+01	18	927	8174	2	Q13332	GDP-Fuc:beta-D-galact	7.21e+01
855	18	0.2	4180	1	N91773	Rat androgen receptor	7.21e+01	18	928	8174	9	Q56908	DNA encoding a glycos	7.21e+01
856	18	0.2	4192	60	X00725	Human aggrecan degrad	7.21e+01	18	929	8174	29	T61677	Human alpha(1,2)-fuco	7.21e+01
857	19	0.2	4199	1	Q05330	Stem cell leukaemia (1.97e+01	18	930	8388	13	Q78191	Vector M48 used for g	7.21e+01
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859	18	0.2	4212	52	V65380	Bovine repeat element	7.21e+01	18	932	9058	41	V10663	Mouse Fas ligand-like	7.21e+01
860	18	0.2	4214	28	T58534	Human connective tiss	7.21e+01	19	933	9096	38	T88015	Human interleukin 16	1.97e+01
861	18	0.2	4221	11	Q64046	A253 derived bcl-1 cD	7.21e+01	18	934	9180	51	V57416	Tumour suppressor gen	1.97e+01
862	18	0.2	4223	44	V22752	Babesia microti BMNI-	7.21e+01	18	935	9299	29	T47716	Mouse bone morphogene	7.21e+01
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865	18	0.2	4234	57	V80596	Kidney injury associa	7.21e+01	18	938	9391	13	Q75164	AF-4 transcript (cDNA	7.21e+01
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868	18	0.2	4253	28	T58361	Tobacco epi-5-aristol	7.21e+01	19	941	9898	42	V20767	Murine Ataxia-telangi	7.21e+01
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872	18	0.2	4382	2	Q12759	P40 genomic DNA.	7.21e+01	19	945	10409	47	V42558	Mouse SRY-related gen	1.97e+01
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874	18	0.2	4481	1	N90958	Sequence encoding ger	7.21e+01	18	947	10475	2	N80643	Mouse dectin-2 gene.	7.21e+01
875	18	0.2	4487	3	Q20514	Encodes germ cell alk	7.21e+01	18	948	10475	1	N80616	Sequence of human pul	7.21e+01
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880	18	0.2	4722	47	V32836	Rabbit low density li	7.21e+01	19	953	11293	19	Q98909	CEA clone HindIII-Sau	7.21e+01
881	19	0.2	4749	28	T59230	FSPI promoter linked	1.97e+01	18	954	11298	34	T86756	TGF-beta responsive e	1.97e+01
882	18	0.2	4771	41	V10354	Murine mTll cDNA.	7.21e+01	18	955	11298	49	V54661	Human high affinity I	7.21e+01
883	19	0.2	5000	47	V38688	Mus musculus SOCS15 c	1.97e+01	18	956	11357	9	Q51024	Human beta subunit of	7.21e+01
884	18	0.2	5009	3	Q21412	Carbonic anhydrase ge	7.21e+01	18	957	12923	3	N90338	Human FCERI beta chai	7.21e+01
885	19	0.2	5053	43	V23127	CDNA of protein with	1.97e+01	19	958	13011	35	T96631	Sequence of human mus	7.21e+01
													cdNA encoding rat cyt	1.97e+01

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C 959 19 0.2 13011 35 T96631 cDNA encoding rat cyt
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C 963 18 0.2 13815 43 V18885 Mus musculus dystroph
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C 970 19 0.2 14704 3 Q20685 PKS 741 insert contg.
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C 974 18 0.2 14985 40 V15693 Human Bin1 gene.
C 975 18 0.2 15056 50 V52967 Carcinoembryonic anti
C 976 18 0.2 15155 3 N50107 DNA encoding Factor-V
C 977 18 0.2 18073 59 V83948 Bacterial artificial
C 978 18 0.2 19307 20 T27558 Shuttle vector pAdDel
C 979 18 0.2 22243 58 V74475 Staphylococcus aureus
C 980 19 0.2 26016 48 V57272 Human flavin-containi
C 981 18 0.2 26698 20 T08126 Mouse syndecan-1 gene
C 982 18 0.2 26700 59 V81283 Mouse syndecan-1 enco
C 983 18 0.2 26700 11 Q67902 Syndecan gene.
C 984 18 0.2 26700 40 V15946 Mouse syndecan gene s
C 985 18 0.2 29392 40 V15422 Mouse poly Ig recepto
C 986 19 0.2 30967 24 T32454 Calpain large subunit
C 987 18 0.2 32026 36 T60559 Recombinant adenoviru
C 988 18 0.2 35000 36 T60557 Recombinant cis-actin
C 989 18 0.2 35100 40 V20441 Human c-fms oncogene.
C 990 18 0.2 40352 40 V02032 MAGE-B cluster DNA se
C 991 19 0.2 40875 33 T80043 Insert from cosmid 10
C 992 18 0.2 53526 40 T94101 Human PKD1 gene.
C 993 18 0.2 53577 28 T18551 Human polycystic kidn
C 994 18 0.2 53577 40 T94108 Human PKD1 locus betw
C 995 18 0.2 80240 59 V83940 NC-contig derived fro
C 996 18 0.2 80595 58 V83939 HC-contig derived fro
C 997 19 0.2 235033 51 V57926 Hereditary haemochrom
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ALIGNMENTS

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RESULT 1
ID T38196 standard; DNA; 7653 BP.
AC T38196;
DI 17-DEC-1996 (first entry)
DE Nematode Ced-3 gene.
KW Ced-3; interleukin-1 beta converting enzyme; ICE; protease;
KW cell death; apoptosis; neural degeneration; inflammation;
KW antiinflammatory; ds.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
FT repeat_unit 1356..1472
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FT 1490..1614
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FT 2167..2366
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PN WO9625946-A1.

PD 29-AUG-1996.

PF 23-FEB-1996; U02473.

PR 24-FEB-1995; US-394189.

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Horvitz HR, Shaham S, Yuan J;

DR WPI; 96-425082/42.

DR P-PSDB; R98754.

PT Ced-3 and human interleukin 1-beta convertase genes and proteins

PT useful to treat inflammation and diseases characterised by cell

PT death

PS Claim 18; Fig 3; 139pp; English.

CC The Caenorhabditis elegans ced-3 gene (T38196) was cloned by
CC mapping RFLPs and chromosome walking, and genomic DNA cloned
CC in plasmid pJ107 was sequenced. EMS-induced alleles were also
CC sequenced. The gene codes for a cell death protein (R98754) that
CC is structurally similar to human interleukin-1 beta converting
CC enzyme (ICE) (R98755), suggesting that Ced-3 protein may be a
CC cysteine protease like ICE and that ICE may be a human equivalent
CC of the nematode cell death gene. The ced-3 gene can be used as a
CC probe or in the prodn. of Ced-3 protein and novel drugs for
CC enhancing or inhibiting the activity of ICE, ced-3 and related
CC genes for the treatment of inflammatory diseases and/or diseases
CC caused by cell death. Novel inhibitors of ced-3 activity include
CC portions of the ced-3 gene and its product.

SQ Sequence 7653 BP; 2429 A; 1456 C; 1270 G; 2498 T;

Query Match 99.6%; Score 7622; DB 24; Length 7653;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 7652; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 agatctgaataaggtgataaataataaataagtgatcttctgaggaatttgactgt 60
QY 1 AGATCTGAATAAGGTGATAAATAATAAATAAGTGATTTCTGAGGAATTTGACTGT 60
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Db 301 ttttctttgttctttttgttgaaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
QY 301 TTTTCTTTGTTCTTTTGTGAAACGTTGCTTAAGCAATTTATTACATCAATTTGAAGAAA 360

Db 361 ggctcgccgatttattgttgccagaaaagattctgagattctcgaagtgcgattttataata 420
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RESULT 2
ID Q54401 standard; DNA; 7653 BP.
AC Q54401;
DT 01-JUL-1994 (first entry)
DE ced-3 gene.
KW C.elegans; cell death; gene; ced-3; inhibition; human; parasite;
KW interleukin-lbeta convertase; ICE; pro-interleukin-lbeta; cytokine;
KW inflammatory response; nematode; diagnosis; myocardial infarction;
KW stroke; degenerative disease; traumatic brain injury; hypoxia; pest;
KW pathogenic infection; hair loss; cancer; autoreactive antibody; ss.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
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FT exon 2232..2366

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FT FT      /number= Intron_3
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FT FT      /*tag= k
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FT FT      23-DEC-1993.
FT FT      14-JUN-1993; U05705.
FT FT      12-JUN-1992; US-897788.
FT FT      20-NOV-1992; US-984182.
FT FT      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT FT      Horvitz HR, Shaham S, Yuan J;
FT FT      WPI; 94-007551/01.
FT FT      P-PSDB; R45262.
FT FT      Agents which affect activity of cell death genes - used to
FT FT      develop drugs for treating conditions characterised by cell death
FT FT      or proliferation
FT FT      Disclosure; Fig 3; 132pp; English.
FT FT      This sequence encodes the C.elegans cell death gene, ced-3. Fragments
FT FT      of the amino terminal of the protein encoded by this sequence act as
FT FT      inhibitors of ced-3. This gene has considerable similarity to human
FT FT      interleukin-1beta convertase (ICE), which converts pro-interleukin-
FT FT      1beta to the active cytokine and is involved in inflammatory response
FT FT      in humans. The similarity between the two sequences suggests that
FT FT      inhibitors of ced-3 may also act as inhibitors of ICE. Human ICE and
FT FT      nematode Ced-3 proteins have an overall amino acid similarity of 28%.
FT FT      The ced-3 inhibitors may be used for identifying agents which affect
FT FT      the activity of a gene belonging to the to the ced-3/ICE family of
FT FT      genes and for diagnosis of diseases characterised by cell death. They
FT FT      can also be used to develop drugs for treating conditions characterised
FT FT      by cell deaths such as myocardial infarction, stroke, degenerative
FT FT      disease, traumatic brain injury, hypoxia, pathogenic infection, or
FT FT      hair loss, or drugs for reducing the proliferative capacity or size
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CC of a population of cells such as cancerous cells, cells which produce
CC autoreactive antibodies, infected cells, hair follicle cells or cells
CC which are critical to the life of a parasite, pest or recombinant
CC organism. They may also be used in the diagnosis of inflammatory
CC disease.
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;

Query Match 96.8%; Score 7405; DB 9; Length 7653;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 7645; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 4

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AC Q64741;
DT 23-JUN-1994 (first entry)
DE ced-3 (G6372A) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
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RESULT 5
ID Q64742 standard; DNA; 7653 BP.
AC Q64742;
DT 23-JUN-1994 (first entry)
DE ced-3 (C6434T) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
FT repeat_unit 1356..1472
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FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t repeat at 1490-1614"
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FT exon 2232..2366
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FT intron 2367..2429
FT /*tag= d
FT /number= Intron_1
FT exon 2450..2575
FT /*tag= e
FT /number= Exon_2
FT intron 2576..2853
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FT intron 3108..4302
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FT /*tag= x
FT /number= Intron_7
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FT /*tag= y
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FT /number= Exon_8

PN W09325685-A.
PD 23-DEC-1993.
PF 14-JUN-1993; U05701.
PR 12-JUN-1992; US-897788.
PR 20-NOV-1992; US-979638.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Horvitz HR, Shaham S, Yuan J;

DR WPI; 94-007542/01.
DR P-PSDB; R53285.
PT Isolated C elegans cell death genes ced-3 and ced-4 - used to
PT develop agents to increase or prevent cell death in organisms
PS Claim 14; Fig 4; 127pp; English.
CC The sequences given in Q64735-45 represent mutations of the C. elegans
CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other C. elegans genes, such
CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;
Query Match 93.1%; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Db 1 agatctgaataaggtgataaataataataaataagtgattttcaggaatttgactgt 60
QY 1 AGATCTGAATAAGGTGATAAATAATAATAAATAAGTGATTTCAGGAATTGACTGT 60
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RESULT 7
ID Q64743 standard; DNA: 7653 BP.
AC Q64743;
DT 23-JUN-1994 (first entry)
DE ced-3 (C6485T) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
FT repeat_unit 1356..1472
FT /tag= a
FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t repeat at 1490-1614"
FT repeat_unit 1490..1614
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FT /note= "Inverted w.r.t. repeat at 1356-1472"
FT exon 232..2366
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FT intron 2367..2429
FT /tag= d
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FT PD 23-DEC-1993.
FT PE 14-JUN-1993; U05701.
FT PR 12-JUN-1992; US-897788.
FT PR 20-NOV-1992; US-979638.
FT PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT PI Horvitz HR, Shaham S, Yuan J;
FT DR WPI; 94-007542/01.
FT DR P-PSDB; R53286.
FT PT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT PT develop agents to increase or prevent cell death in organisms
FT PS Claim 14; Fig 4; 127pp; English.
FT CC The sequences given in Q64735-45 represent mutations of the C. elegans

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CC CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC CC was most abundant in embryos, but was also detected in larvae and young
CC CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC CC cell death. The four largest introns as well as sequences 5' of the
CC CC start codon contain repetitive elements, some of which have been
CC CC characterised in non-coding regions of other C. elegans genes, such
CC CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC CC region that might be a transmembrane region. One region of Ced-3 is
CC CC very rich in serine. It is thought that this region is involved in
CC CC protein-protein interactions, similar to acid blobs in transcription
CC CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC CC the mutations are missense mutations, two are nonsense mutations and
CC CC two are putative splicing mutations. These mutations establish the
CC CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC CC function is not essential for viability. The ced-3 and ced-4 gene
CC CC products may be used to develop agents for treating conditions
CC CC characterised by cell deaths, such as myocardial infarction, stroke,
CC CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC CC infection, aging or hair loss.
CC CC
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;

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Query Match 93.1%; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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RESULT 8

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ID Q64740 standard; DNA; 7653 BP.
AC Q64740;
DC 23-JUN-1994 (first entry)
DE ced-3 (C6322T) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
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FT PI Horvitz HR, Shaham S, Yuan J;
FT DR WPI; 94-007542/01.
FT DR P-PSDB; R53283.
FT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT develop agents to increase or prevent cell death in organisms
FT PS Claim 14; Fig 4; 127pp; English.
FT CC The sequences given in Q64735-45 represent mutations of the C. elegans
FT CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT CC was most abundant in embryos, but was also detected in larvae and young
FT CC adults, suggesting that ced-3 is expressed not only in cells undergoing

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PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Horvitz HR, Shaham S, Yuan J;
DR WPI; 94-007542/01.
DR P-PSDB; R53281.
PT Isolated C elegans cell death genes ced-3 and ced-4 - used to
PT develop agents to increase or prevent cell death in organisms
PS Claim 14; Fig 4; 127pp; English.
CC The sequences given in Q64735-45 represent mutations of the C. elegans
CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other C. elegans genes, such

CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of
CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
SQ Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T;

Query Match 93.1%; Score 7126; DB 9; Length 7653;
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RESULT 10

ID Q64745 standard; DNA; 7653 BP.
AC Q64745;
DT 23-JUN-1994 (first entry)
DE ced-3 (C7020T) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
FT repeat_unit 1356..1472
FT /*tag= a
FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 1490-1614"
FT repeat_unit 1490..1614
FT /*tag= b
FT /rpt_type= INVERTED
FT /note= "Inverted w.r.t. repeat at 1356-1472"
FT exon 2232..2366
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FT /number= Exon_1
FT intron 2367..2429
FT /*tag= d
FT /number= Intron_1
FT exon 2450..2575
FT /*tag= e
FT /number= Exon_2
FT intron 2576..2853
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FT exon 2854..3107
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FT /number= Exon_3
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FT /note= "C>T, from allele n1163"
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PN W09325685-A.
PD 23-DEC-1993.
PF 14-JUN-1993; U05701.
PR 12-JUN-1992; US-897788.
PR 20-NOV-1992; US-979638.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Horvitz HR, Shaham S, Yuan J;
DR WPI; 94-007542/01.
DR P-PSDB; R53288.
PT Isolated C elegans cell death genes ced-3 and ced-4 - used to
PT develop agents to increase or prevent cell death in organisms
PS Claim 14; Fig 4; 127pp; English.
CC The sequences given in Q64735-45 represent mutations of the C. elegans
CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other C. elegans genes, such
CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is

very rich in serine. It is thought that this region is involved in protein-protein interactions, similar to acid blobs in transcription factors. Of the mutations which occur within the ced-3 gene, eight of the mutations are missense mutations, two are nonsense mutations and two are putative splicing mutations. These mutations establish the null phenotype of the ced-3 gene, confirming that ced-3, like ced-4, function is not essential for viability. The ced-3 and ced-4 gene products may be used to develop agents for treating conditions characterised by cell deaths, such as myocardial infarction, stroke, degenerative disease, traumatic brain injury, hypoxia, pathogenic infection, aging or hair loss.

SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;

Query Match 93.1%; Score 7126; DB 9; Length 7653;
 Best Local Similarity 99.8%; Pred. No. 0.00e+00;
 Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps

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Db	61	tttagcagaattaatctgttttcagaaaaaaagtcaggtttctagatttttccgtctta	120
QY	61	TTTAGCACAAATTAATCTGTTTCAGAAAAAAGTCCAGTTTCTAGATTTTTCCGTCCTTA	120
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QY	121	TTGTGCAATTAATATCCGTATTATCACTTTTTCATGCTCATCTCTCGAGGGCACGTCCTC	180
Db	181	aaagaattgtgagagcaaacgcgtcccatgacctccacactcagcgcgcaaaacaaac	240
QY	181	AAAGAATTGTGAGAGCAACACGCGCTCCCATTTGACCTCCACACTCAGCCGCCAAAAACAAC	240
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QY	241	GTTCGAACATTCGTGTGTGTGCTCCTTTTCCGTTATCTTGCACTCATCTTTTGTGCTTT	300
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QY	301	TTTTCTTTGTTCTTTTGTGAACGTGTTGCTAAGCAATTATTACATCAATTGAGAAAAA	360
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QY	481	TAGTTTACTAATAAAACTACTTTTAAACCTTTACCTTTACCTCACCGCTCCGTTTCATG	540
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QY	1981	TTCAAGAGGGTCAAAATTTCCGATTTTACT	GACTTTTCACTTTTCACTTTTTCGTAGTTCA	2040
Db	2041	gcagttgttgaggatTTTTTGACGAaaaact	tagggaaaaaatcgataaaaaattactcaaatcg	2100
QY	2041	GCAGTTGTTGGAGTTTGTACGAAAAC	TAGGAAAAAATCGATAAAAAATTACTCAAATCG	2100
Db	2101	agctgaattttgaggacaatgtttaaaaaaaaa	cacctatttttccaataatttcactcat	2160
QY	2101	AGCTGAATTTTGAGGACAATGTTTAAAAA	AAAAAACACTATTTTCCAATAATTCTACTCAT	2160
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QY	2221	ATCAGCCGAAGATGATCGGTCAAGATAGA	AGGAGCTTGCTAGAGAGGAACATTATGATGT	2280
Db	2281	tctctagtcattctaaaagtcgatgaaat	tctcgaagttctcatcgcgaaaaaacaaagtgtga	2340
QY	2281	TCTCTAGTCATCTAAAGTCGATGAAAT	TCTCGAAGTTCTCATCGCAAAAACAAGTGTGA	2340
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QY	2341	ATAGTGATAATGGAGATATGATTAATGT	GAGTTTTTAATCGAATAATAATTTTAAAAAAA	2400
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QY	2401	AATTGATAATATAAAGAATAATTTT	TTCAGTCAATGTGGAACGGTTTCGCGAGA	2460
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RESULT 11
ID Q64736 standard; DNA; 7653 BP.
AC Q64736;
DT 23-JUN-1994 (first entry)
DE ced-3 (G2487A) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
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FT /note= "Inverted w.r.t repeat at 1490-1614"
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PN WO9325685-A.
PD 23-DEC-1993.
PF 14-JUN-1993; U05701.
PR 12-JUN-1992; US-897788.
PR 20-NOV-1992; US-979638.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Horvitz HR, Shaham S, Yuan J;
DR WPI; 94-007542/01.
DR P-PSDB; R53280.
PT Isolated C elegans cell death genes ced-3 and ced-4 - used to
PT develop agents to increase or prevent cell death in organisms
PS Claim 14; Fig 4; 127pp; English.
CC The sequences given in Q64735-45 represent mutations of the C. elegans
CC ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
CC was most abundant in embryos, but was also detected in larvae and young
CC adults, suggesting that ced-3 is expressed not only in cells undergoing
CC cell death. The four largest introns as well as sequences 5' of the
CC start codon contain repetitive elements, some of which have been
CC characterised in non-coding regions of other C. elegans genes, such
CC as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
CC length. Ced-3 is highly hydrophilic with no significant hydrophobic
CC region that might be a transmembrane region. One region of Ced-3 is
CC very rich in serine. It is thought that this region is involved in
CC protein-protein interactions, similar to acid blobs in transcription
CC factors. Of the mutations which occur within the ced-3 gene, eight of

CC the mutations are missense mutations, two are nonsense mutations and
CC two are putative splicing mutations. These mutations establish the
CC null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
CC function is not essential for viability. The ced-3 and ced-4 gene
CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
SQ Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T;

Query Match 93.1%; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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RESULT 12
ID Q64739 standard; DNA; 7653 BP.
AC Q64739;
DT 23-JUN-1994 (first entry)
DE ced-3 (G6297A) gene.
KW C. elegans; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
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FT 14-JUN-1993; U05701.
FT 12-JUN-1992; US-897788.
FT 20-NOV-1992; US-979638.
FT (MASI ) MASSACHUSETTS INST TECHNOLOGY.
FT Horvitz HR, Shaham S, Yuan J;
FT WPI; 94-007542/01.
FT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT develop agents to increase or prevent cell death in organisms
FT Claim 14; Fig 4; 127pp; English.
FT The sequences given in Q64735-45 represent mutations of the C. elegans
FT ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT was most abundant in embryos, but was also detected in larvae and young
FT adults, suggesting that ced-3 is expressed not only in cells undergoing
FT cell death. The four largest introns as well as sequences 5' of the
FT start codon contain repetitive elements, some of which have been
FT characterised in non-coding regions of other C. elegans genes, such
FT as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
FT length. Ced-3 is highly hydrophilic with no significant hydrophobic
FT region that might be a transmembrane region. One region of Ced-3 is
FT very rich in serine. It is thought that this region is involved in
FT protein-protein interactions, similar to acid blobs in transcription
FT factors. Of the mutations which occur within the ced-3 gene, eight of
FT the mutations are missense mutations, two are nonsense mutations and
FT two are putative splicing mutations. These mutations establish the
FT null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
FT function is not essential for viability. The ced-3 and ced-4 gene
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CC products may be used to develop agents for treating conditions
CC characterised by cell deaths, such as myocardial infarction, stroke,
CC degenerative disease, traumatic brain injury, hypoxia, pathogenic
CC infection, aging or hair loss.
SQ Sequence 7653 BP; 2430 A; 1453 C; 1271 G; 2499 T;

Query Match 93.1%; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db	661	accactccatcacctcttttggcgggtgttcttcgaaacccacttaggaaagcagtggtat	720
QY	661	ACCACTCCATCACCTCTTTGGCGGTGTTCTTCGAAACCCACTTAGGAAAGCAGTGTAT	720
Db	721	ctcatttggtatgctcttttgcatttttatagctcttttgcgaatttcaatgtcttaaac	780
QY	721	CTCAFTTGGTATGCTCTTTTCGATTTTATAGCTCTTTGCGCAATTTCAATGCTTTAAAC	780
Db	781	aatcaaatcgcatattattgtgcatggaggaataatgacggggttggaattcttagatga	840
QY	781	AATCCAAATCGCATTATATTGTGCATGGAGGCAAAATGACGGGTTGGAATCTTAGATGA	840
Db	841	gacaggagctttcagggttaacgcccggttcattttgtaccacatttcatcatttccct	900
QY	841	GATCAGAGCTTTCAGGGTAAACGCCCGGTTCAATTTGTACCACATTTTCATCATTTTCT	900
Db	901	gtcgtccttggtatcctcaactgtccccggttttgttttcggttacactcttccgtgatgc	960
QY	901	GTCTGCTTGGTATCTCTCAACTGTGTCGGGTTTTGTTTTTCGGTACACTCTTCCGTTATGC	960

Db	961	caccgtctccgtctcaattatcggttagaaaaatgaaactgtccagatgggtgactcata	1020
QY	961	CACCTGTCTCCGTCTCAATATATCGTTTAGAAATGTGAACGTGTCCAGATGGGTGACTCATA	1020
Db	1021	ttgtgctgtctacaatccacttttctctcatcgcgagtccttacgagcccatcataaac	1080
QY	1021	TTGTGCTGTCTACAATCCACTTCTTTTCTCATCGCGAGTCTTACGAGCCCATATAAAC	1080
Db	1081	tttttttccgcggaatttgcataaaacccggccaaaaaactttctccaaattgttacgcaa	1140
QY	1081	TTTTTTTCCGGGAAATTTGCAATAAACCCGCCAAAAAATTTCTCCAAATTTGTAGCGCAA	1140
Db	1141	tatatcaaatccataagaatatctctcaatgttttatgatttcttcgcagcactttctct	1200
QY	1141	TATATACAATCCATAAGAATATCTTCTCAATGTTTATGATTTCTTCGACACTTTCTCT	1200
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QY	1201	TCGTGTCTAACATCTTATTTTATAATATTTCCGCTAAAAATCCGATTTTGTAGTATTA	1260
Db	1261	atttatcgtaaaattatgataatagcaccgaaactactaaaaaaggtaaaagctccttt	1320
QY	1261	ATTTATCGTAAATTTATCATATAATAGCACCGAAAACTACTAAAAATGGTAAAGCTCTTT	1320
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QY	1321	TAAATCGGCTCGACATTATCGTATTAGGAATCACAAAAATCTGAGAAATGCGTACTGCGC	1380
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QY	1381	AACATATTGACGGCAAAATATCTCGTAGCGAAACTACAGTAATTTCTTTAAATGACTAC	1440
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QY	1441	TGTAGCGCTGTGTGCGATTACGGGCTCAATTTTGAATAAATAATTTTTCGAAATTT	1500
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QY	1501	TGATAACCGTAAATCGTCAACACGCTACAGTAGTCAATTAAAGGATTACTGTAGTCTA	1560
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QY	1621	TCCGTAAATAATTTCAACAAGATTTTGGCATTTCCACTTTAAAGGCGCACAGGATTTATCCA	1680
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QY	1681	ATGGGTCTCGGCACGCAAAAAGTTTGATAGACTTTTAAATTTCTCTTGCATTTTAAATTC	1740
Db	1741	aattactaaaaatttctgtgaatttttctgttaaaatttttaaataatcagtttttctaattt	1800
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RESULT 13
ID Q64738 standard; DNA; 7653 BP.
AC Q64738;
DT 23-JUN-1994 (first entry)
DE ced-3 (C5940T) gene.
KW C. elegans; ced-4; ced-3; mutant; transcriptional regulation;
KW embryogenesis; cell death; hydrophilic; transmembrane; region;
KW hydrophobic; mutation; amino acid; substitution; RNA splicing;
KW protein synthesis; null phenotype; calcium-binding domain; ss.
OS Caenorhabditis elegans.
FH Location/Qualifiers
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FT W09325685-A.
FT 23-DEC-1993.
FT 14-JUN-1993; U05701.
FT 12-JUN-1992; US-897788.
FT 20-NOV-1992; US-979638.
FT (MASI) MASSACHUSETTS INST TECHNOLOGY.
FT Horvitz HR, Shaham S, Yuan J;
FT WPI; 94-007542/01.
FT P-PSDB; R53282.
FT Isolated C elegans cell death genes ced-3 and ced-4 - used to
FT develop agents to increase or prevent cell death in organisms
FT Claim 14; Fig 4; 127pp; English.
FT The sequences given in Q64735-45 represent mutations of the C. elegans
FT ced-3 gene. A 2.8 kb mRNA was identified as the ced-3 transcript and
FT was most abundant in embryos, but was also detected in larvae and young
FT adults, suggesting that ced-3 is expressed not only in cells undergoing
FT cell death. The four largest introns as well as sequences 5' of the
FT start codon contain repetitive elements, some of which have been
FT characterised in non-coding regions of other C. elegans genes, such
FT as fem-1, lin-12 and myoD. The Ced-3 protein is 503 amino acids in
FT length. Ced-3 is highly hydrophilic with no significant hydrophobic
FT region that might be a transmembrane region. One region of Ced-3 is
FT very rich in serine. It is thought that this region is involved in
FT protein-protein interactions, similar to acid blobs in transcription
FT factors. Of the mutations which occur within the ced-3 gene, eight of
FT the mutations are missense mutations, two are nonsense mutations and
FT two are putative splicing mutations. These mutations establish the
FT null phenotype of the ced-3 gene, confirming that ced-3, like ced-4,
FT function is not essential for viability. The ced-3 and ced-4 gene
FT products may be used to develop agents for treating conditions
FT characterised by cell deaths, such as myocardial infarction, stroke,
FT degenerative disease, traumatic brain injury, hypoxia, pathogenic

CC infection, aging or hair loss.
SQ Sequence 7653 BP; 2429 A; 1452 C; 1272 G; 2500 T;
Query Match 93.1%; Score 7126; DB 9; Length 7653;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 7636; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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QY 1 AGATCTGAAATAAGGTGATAAATTAATAAATTAAGTGTATTTCTGAGGAAATTTGACTGT 60
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Db 4921 ttctgaattttcaaaaattatccaaaaatgcacaaatttaaaatttgcgaaaattggcaaac 4980
QY 4921 TTCTGAATTTTCAAAATTTATCCAAAAATGCACAAATTTTAAATTTGTGAAAAATTTGGCAAC 4980
Db 4981 ggtgtttcacaatatgaaatgtatttttaaaaactttaaaaaccactccggaaaaagcaataa 5040
QY 4981 GGTGTTTCAATATGAATGTATTTTAAAAAATTTTAAAAAACCCTCCGGAAAAAGCAATAA 5040
Db 5041 aaatcaaaaacagtcacaaattcaaaattcaaaagtattcatccgatttgcatttttg 5100
QY 5041 AAATCAAAAACAGTCACAATTCAAATTCAAAAGTTATTTCATCCGATTGTGTTATTATTG 5100
Db 5101 caaaatttgaaaaaatcatgaagatttagaaaaagttttataacatttttcttagatttt 5160
QY 5101 CAAAAATTTGAAAAAATCATGAAGGATTTAGAAAAAGTTTTTATAACATTTTTTCTAGATTTT 5160
Db 5161 tcaaaatttttttaaaaaatcgagaaaaagagaatgaaaaatcgatttttaaaatatcc 5220
QY 5161 TCAAAATTTTAAAAATCGAGAAAAAGAGAAATGAAAAATCGATTTTAAAAATATCC 5220
Db 5221 acagcttcgagagtttgaaaattacagtactccttaaggcgacaccccatgttcattgg 5280
QY 5221 ACAGCTTCGAGAGTTTGAAATTTACAGTACTCCTTAAAGGCGCACACCCCATTTGCATTGG 5280
Db 5281 accaaaaatttgcgtgcgagaccaggtaccgtagtttttgcgaaaaaattgcaccat 5340
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Db 5341 tggacaataaaaccttcctaataatcaccacaaaaagtaaaattgaaatcttcgaaaaagccaaaaa 5400

Db 7561 aaatttgtaggtccccccatcatttccccgcccacatctcctcaaaattgcatttcttttttcg 7620
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QY 7561 AAATTGTAGTCCCGCCCATCATTTCCCGCCCATCATCTCAAAATGCAATCTTTTTCG 7620
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Db 7621 cagtcatatcccgattctgtgcagcaaatct 7653
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QY 7621 CCGTGATATCCCGATTCTGTGTCAGCAAAAGATCT 7653
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RESULT 14
ID Q79970 standard; cDNA; 2485 BP.
AC Q79970;
DT 13-SEP-1995 (first entry)
DE Interleukin-1 beta convering enzyme homolog ced3 cDNA.
KW Interleukin-1 beta converitng enzyme; homolog ced3;
KW oncogene bcl-2; programmed cell death; cancer treatment; ss.
OS Caenorhabditis elegans.
FH Key Location/Qualifiers
cds 17..1528
FT /*tag= a
PN WO9500160-A.
PD 05-JAN-1995.
PF 10-JUN-1994; U06630.
PR 24-JUN-1993; US-080850.
PA (GEO) GEN HOSPITAL CORP.
PI Miura M, Yuan J;
DR WPI: 95-051742/07.
DR P-PSDB; R66770.
PT Promoting or preventing programmed cell death in vertebrate cells
PT - by inhibiting the activity of interleukin-1 beta converting
PT enzyme.
PS Example 1; Fig 2C; 116pp; English.
CC Q79970 encodes R66770 interleukin-1 beta converting enzyme homolog
CC ced3, increasing ced3s enzymatic activity can promote the
CC programmed cell death of cancer cells (pref. those overexpressing
CC the bcl-2 oncogene), this can be used as the basis of a new cancer
CC treatment. Alternatively by reducing ced3s enzymatic activity
CC programmed cell death can be inhibited, this may be useful in the
CC development of new cell lines which remain viable in culture for
CC extended or indefinite periods, independant of growth factors.
SQ Sequence 2485 BP; 684 A; 564 C; 480 G; 757 T;

Query Match 6.6%; Score 505; DB 14; Length 2485;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1464 agatgacatccgcctgctcaaaagtctacttttggcgggaagcacgaaactctgccc 1523
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QY 7011 AGATGACATCCCGCTGCTCAAAAGTTCTACTTTTGGCGGAAGCACGAAACTGTCCG 7070
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Db 1524 tctaaattcactcgtgattcattgcccgaattgataattgtctgtatcttctccccagtt 1583
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QY 7071 TCTAAATTCACCTCGTGATTCTATGCCCCAATTGATAATTGTCTGTATCTTCTCCCCAGT 7130
|||||
Db 1584 tctcttgcgcccattagtttaaaaccatgtgtatatattgttatccctatactcatttcaact 1643
|||||
QY 7131 TCTCTTTGCGCCCAATTAGTTTAAACCATGTGTATATTGTTATCTTACTCAATTTCACT 7190
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Db 1644 ttatcatctatcatcttctcttccattttcacacatttccatttctctacgataatcta 1703
|||||
QY 7191 TTATCATTTCTATCATTTCTCTTCCCATTTTCCACACATTTCCATTTCTCTACGATAATCTA 7250
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Db 1704 aaattatgacgtttgtgtctcgaacgcataataattttaataactcgttttgaatttgat 1763
|||||
QY 7251 AAATTATGACGTTTGTGTCTCGAACGCATAATAATTTTAAATAACTCGTTTGAATTGAT 7310
|||||
Db 1764 tagttgtgtgcccagttatatgtatgtactatgctctctatcaacaaaatagtttccata 1823
|||||
QY 7311 TAGTTGTTGTGCCCAGTATATATGTATGTACTATGTCTTCTATCAACAAATAGTTTCATA 7370
|||||
Db 1824 gatcatcaccccaacccccaccacacccaccgtaccatattcatttttgcgggaatcaatt 1883
|||||
QY 7371 GATCATCACCCCAACCCCAACCAACCTACCGTACCATATTCTATTTTGGCGGAATCAATT 7430
|||||

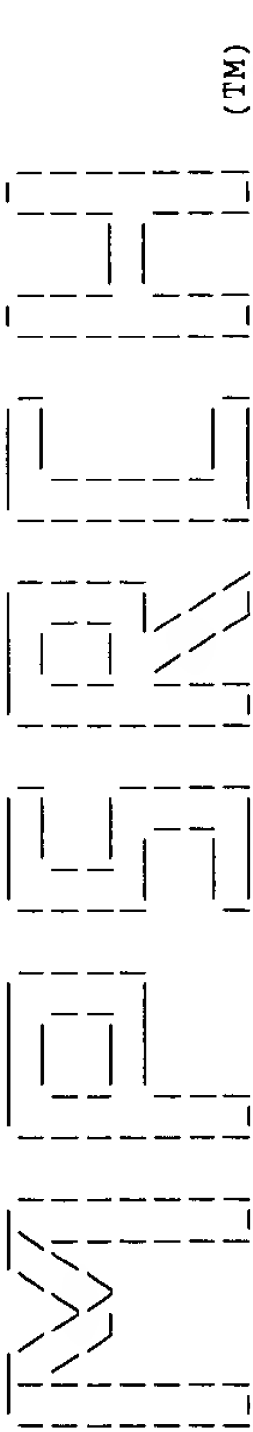
Db 1884 tcgattaaatttaaacctatttttccgcacaaaaaatctaatatttgaattaacgaatag 1943
|||||
QY 7431 TCGATTAAATTTAACCTATTTTTCGCCACAAAAAATCTAATATTGTAATTAACGAATAG 7490
|||||
Db 1944 cattcccatctctcccggtgcggaa 1968
|||||
QY 7491 CATTCCTCATCTCTCCCGTGCCTGGAA 7515
|||||

RESULT 15
ID Q54629 standard; DNA; 6560 BP.
AC Q54629;
DT 23-JUN-1994 (first entry)
DE Genomic region containing ced-9 gene.
KW Cell death; senescence; programmed cell death; ced-9; myocardial
KW infarction; stroke; brain injury; neurodegenerative disease;
KW muscular degenerative disease; ageing; hypoxia; ischaemia; toxemia;
KW infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
KW oncogene; ss.
OS Caenorhabditis elegans.
PN WO9325683-A.
PD 23-DEC-1993.
PF 14-JUN-1993; U05651.
PR 12-JUN-1992; US-898933.
PR 10-AUG-1992; US-927681.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PI Hengartner M, Horvitz HR;
DR WPI: 94-007540/01.
PT Caenorhabditis elegans cell death-protective gene - used to
PT develop agents for preventing cell death or for reducing
PT population of cells
PS Claim 3; Page 54-58; 112pp; English.
CC ced-9 is essential for C. elegans development and apparently
CC functions by protecting cells during development from programmed
CC cell death. ced-9 was shown to function by antagonising the
CC activities of cell death genes ced-3 and ced-4. The protein product
CC of the human oncogene bcl-2 was found to have a similar sequence
CC to the ced-9 protein. The ced-9 gene can be used for developing
CC agents for treating a condition characterised by increased cell death
CC such as myocardial infarction, stroke, traumatic brain injury,
CC neurodegenerative disease, muscular degenerative disease, ageing,
CC hypoxia, ischaemia, toxemia, infection or hair loss. It can also
CC be used for reducing a population of cells in the treatment of
CC neoplastic growth cancerous tissue, infected cells or autoreactive
CC immune cells.
SQ Sequence 6560 BP; 2040 A; 1274 C; 1203 G; 2023 T;

Query Match 0.5%; Score 39; DB 9; Length 6560;
Best Local Similarity 100.0%; Pred. No. 1.18e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3249 catttaaagaattactgtagtttttcgctacgagatatatt 3287
|||||
Cp 1435 CATTTAAGAATTACTGTAGTTTTCGCTACGAGATATTT 1397
|||||

Search completed: Mon Aug 9 00:52:07 1999
Job time : 1704 secs.



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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sun Aug 8 20:50:46 1999; MasPar time 12577.83 Seconds
Tabular output not generated. 1425.700 Million cell updates/sec

Title: >US-08-287-669-18
Description: (1-7653) from US08287669.seq (10 of 10)
Perfect Score: 7653
N.A. Sequence: 1 AGATCTGAAATAAGGTGATA.....ATTCTGTCAGCAAGATCT 7653
Comp: TCTAGACTTTATTCACATAT.....TAAGACCAGTCGTTCTAGA

Scoring table: TABLE jmetric
Gap 60
Nmatch STD : Dbase 0; Query 0
Searched: 2883791 seqs, 1171580779 bases x 2
Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database: embl-est58
1:em_est10 2:em_est11 3:em_est17 4:em_est18 5:em_est2
6:em_est9 7:em_gss1
Database: genbank-est11
8:gb_est1 9:gb_est10 10:gb_est11 11:gb_est12 12:gb_est13
13:gb_est14 14:gb_est15 15:gb_est16 16:gb_est17
17:gb_est18 18:gb_est19 19:gb_est20 20:gb_est21
21:gb_est22 22:gb_est23 23:gb_est24 24:gb_est25
25:gb_est26 26:gb_est27 27:gb_est28 28:gb_est29
29:gb_est30 30:gb_est31 31:gb_est32 32:gb_est33 33:gb_est34
34:gb_est35 35:gb_est36 36:gb_est37 37:gb_est38 38:gb_est39
39:gb_gss3 40:gb_gss4 41:gb_gss5 42:gb_gss6

Statistics: Mean 10.997; Variance 1.798; scale 6.117
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Result No.	Score	Query Match	Description		
C 1	299	3.9	C38304 Yuji Kohara unp	0.00e+00	
2	198	2.6	CELK105H1F Yuji Kohara	0.00e+00	
3	177	2.3	C39290 Yuji Kohara unp	0.00e+00	
4	153	2.0	C51090 Yuji Kohara unp	1.03e-296	
5	29	0.4	C29898 Yuji Kohara unp	5.37e-15	
6	29	0.4	CELK086D2R Yuji Kohara	5.37e-15	
7	31	0.4	WEST01956 Early embryo	2.09e-18	
8	28	0.4	C50455 Yuji Kohara unp	2.43e-13	
9	27	0.4	CELK098H4F Yuji Kohara	1.01e-11	
C 10	21	0.3	CSRL-131f8-u CSRL flow	6.31e-03	

84	20	0.3	281	8	T16338	NIB1146 Normalized inf	1.19e-01	157	20	0.3	345	40	AQ236593	RPC111-68C13.TK RPC111	1.19e-01
85	20	0.3	281	33	N98071	2160C3 czapFDD2.1, De	1.19e-01	158	20	0.3	346	21	AI007409	TENU0429 T.cruzi epima	1.19e-01
86	23	0.3	283	19	F04162	HSC2LB112 normalized i	1.17e-05	159	20	0.3	346	18	AA772976	af33h12.s1 Soares_tota	1.19e-01
87	21	0.3	284	35	AQ097550	HS_3039_B2_A08_MR CIT	6.31e-03	160	20	0.3	346	8	T02792	0134M3 gmbPfHB3.1, G.	1.19e-01
88	21	0.3	285	15	AA596726	vm60g07.r1 Stratagene	6.31e-03	161	20	0.3	346	34	W97983	mg06b04.r1 Soares mous	1.19e-01
89	20	0.3	285	38	AQ070538	HS_2266.A2_H07_MR CIT	1.19e-01	162	21	0.3	347	21	AI013289	EST207964 Normalized r	6.31e-03
90	24	0.3	286	8	Z40981	HSC2LB122 normalized i	4.19e-07	163	20	0.3	347	42	AQ442968	HS_5055_B2_G03_SP6E RP	1.19e-01
91	21	0.3	286	11	AA302775	EST10463 Adipose tissu	6.31e-03	164	20	0.3	348	28	AI504555	vol0h09.x1 Barstead mo	1.19e-01
92	20	0.3	286	24	AA680971	to0ld02.x1 NCI_CGAP_Ut	1.19e-01	165	21	0.3	349	42	AQ419159	RPC1-11-179N17.TV RPCI	6.31e-03
93	20	0.3	290	28	AA680971	LmFrAm0589 Leishmania	1.19e-01	166	20	0.3	349	27	AI462927	vb86g08.x1 Soares mous	1.19e-01
94	20	0.3	291	23	AI111609	UI-R-C2-rm-e-10-0-UI.s	1.19e-01	167	21	0.3	350	14	AA492908	vi80e07.r1 Stratagene	6.31e-03
95	20	0.3	291	20	AA902486	ok91g08.s1 NCI_CGAP_Lu	1.19e-01	168	21	0.3	350	22	AI090268	qb28e10.x1 Soares_preg	6.31e-03
96	21	0.3	293	27	AA988318	UI-R-C0-ia-c-08-0-UI.s	6.31e-03	169	20	0.3	353	35	D44824	HUMSUPY276 Human brain	1.19e-01
97	20	0.3	294	32	H87782	ys75d08.s1 Soares reti	1.19e-01	170	21	0.3	354	38	B94008	CIT-HSP-2168J22.TF CIT	6.31e-03
98	20	0.3	295	37	FR0011335	F.rubripes GSS sequenc	1.19e-01	171	21	0.3	354	33	W09051	ma69h08.r1 Soares mous	6.31e-03
99	20	0.3	299	36	C21893	C21893 Valencia orange	1.19e-01	172	22	0.3	354	25	AI322082	SWOV3MCAM12B12SK Oncho	2.90e-04
100	21	0.3	299	13	AA457251	aa91e05.s1 Stratagene	6.31e-03	173	21	0.3	354	39	AQ220375	HS_3242_B2_G07_T7 CIT	6.31e-03
101	21	0.3	300	35	AQ100181	HS_3049_B2_F10_MR CIT	6.31e-03	174	20	0.3	354	26	AA859059	UI-R-A0-ak-e-10-0-UI.s	1.19e-01
102	20	0.3	300	15	C29898	C29898 Yuji Kohara unp	1.19e-01	175	20	0.3	354	34	AQ220375	CIT-HSP-2314J13.TF CIT	1.19e-01
103	26	0.3	300	15	C32017	C32017 Yuji Kohara unp	3.86e-10	176	20	0.3	355	38	W69992	zd51a10.r1 Soares_feta	1.19e-01
104	26	0.3	300	15	C37964	C37964 Yuji Kohara unp	3.86e-10	177	22	0.3	357	15	C41501	C41501 Yuji Kohara unp	1.19e-01
105	24	0.3	300	15	C52036	C52036 Yuji Kohara unp	4.19e-07	178	20	0.3	357	39	AQ112823	CIT-HSP-2371F21.TF CIT	1.19e-01
106	20	0.3	300	15	C34591	C34591 Yuji Kohara unp	1.19e-01	179	23	0.3	357	15	C41501	Y564C04.s1 Soares reti	1.19e-05
107	20	0.3	300	41	AQ316539	CIT-HSP-2384L16.TFB CI	1.19e-01	180	20	0.3	358	37	B77399	Y564C04.s1 Soares reti	1.19e-01
108	20	0.3	301	27	AA957697	UI-R-El-fw-g-03-0-UI.s	1.19e-01	181	20	0.3	358	37	B77399	T3009TFC TAMU Arabidop	1.19e-01
109	20	0.3	303	12	AA379146	EST92195 Skin tumor I	1.19e-01	182	20	0.3	358	40	AQ265549	RPC111-76C24.TJ RPC111	1.19e-01
110	23	0.3	304	26	AI399740	th28h05.x1 NCI_CGAP_Pr	1.17e-05	183	21	0.3	359	8	T00037	wEST00758 Early embryo	6.31e-03
111	20	0.3	304	24	AU034595	AU034595 Dictyostelium	1.19e-01	184	26	0.3	360	15	C50455	C50455 Yuji Kohara unp	3.86e-10
112	23	0.3	304	24	AU034595	qh76a10.x1 Soares_feta	1.17e-05	185	22	0.3	360	15	C64964	C64964 Yuji Kohara unp	2.90e-04
113	20	0.3	306	30	R46062	Yg47h06.s1 Soares inf	1.19e-01	186	22	0.3	360	32	D67664	CELK076C9F Yuji Kohara	2.90e-04
114	20	0.3	307	24	AI225900	ui23b06.y1 Soares sequ	1.19e-01	187	22	0.3	360	15	C62642	C62642 Yuji Kohara unp	2.90e-04
115	20	0.3	309	37	FR0028277	Fugu rubripes GSS sequ	1.19e-01	188	21	0.3	360	32	D70300	CELK100C2F Yuji Kohara	6.31e-03
116	20	0.3	310	10	AA297749	EST113320 Infant brain	1.19e-01	189	21	0.3	360	32	D70300	CELK101EXF Yuji Kohara	6.31e-03
117	20	0.3	311	24	AI273970	qu84a05.x1 NCI_CGAP_Ga	1.19e-01	190	20	0.3	360	19	F06515	HSC1AG041 normalized i	1.19e-01
118	24	0.3	314	8	T02201	wEST02922 Early embryo	4.19e-07	191	20	0.3	360	40	AQ254763	EP(X)1232 Drosophila m	1.19e-01
119	20	0.3	314	15	AA608686	ae55g12.s1 Stratagene	1.19e-01	192	20	0.3	360	15	C68005	C68005 Yuji Kohara unp	1.19e-01
120	20	0.3	314	39	B86304	RPC111-22K17.TV RPC111	1.19e-01	193	20	0.3	361	31	H56539	Yt88g07.r1 Soares_pine	1.19e-01
121	21	0.3	315	33	W11688	mb17b06.r1 Soares mous	6.31e-03	194	21	0.3	362	39	B89390	RPC111-27G9.TPB RPC111	6.31e-03
122	20	0.3	315	17	AA741717	LmLv39p3/349B Leishman	1.19e-01	195	21	0.3	362	23	AI175024	EST218542 Normalized r	6.31e-03
123	20	0.3	316	38	B70969	CIT-HSP-2063I12.TR CIT	1.19e-01	196	21	0.3	362	20	C84227	C84227 Dictyostelium d	6.31e-03
124	20	0.3	317	12	AA348720	EST55215 Hippocampus I	1.19e-01	197	21	0.3	363	21	AA985341	am79h05.s1 Stratagene	6.31e-03
125	21	0.3	317	28	AI508356	vx46g11.y1 Stratagene	6.31e-03	198	20	0.3	364	39	AQ085109	HS_2268.A1_C05_MF CIT	1.19e-01
126	20	0.3	317	19	R21668	Yg50a12.r1 Soares inf	1.19e-01	199	20	0.3	365	22	AI100430	34805 Lambda-PRL2 Arab	1.19e-01
127	20	0.3	319	16	AA647096	vn39f05.r1 Stratagene	1.19e-01	200	20	0.3	366	27	AI440044	ti98h12.x1 NCI_CGAP_Ga	1.19e-01
128	20	0.3	319	35	C14190	C14190 Clontech human	1.19e-01	201	20	0.3	367	34	W52069	zc47d12.r1 Soares_sene	1.19e-01
129	20	0.3	320	39	AQ100859	HS_3060.A1_E05_MR CIT	1.19e-01	202	20	0.3	369	12	AA389959	vb30a04.r1 Soares mous	1.19e-01
130	20	0.3	320	35	AA063349	zm04b09.s1 Stratagene	1.19e-01	203	20	0.3	369	26	AA819575	UI-R-A0-bh-f-09-0-UI.s	1.19e-01
131	20	0.3	321	37	FR0006855	F.rubripes GSS sequenc	1.19e-01	204	20	0.3	369	8	T02008	wEST02729 Early embryo	1.19e-01
132	20	0.3	321	34	AA001264	zh82d06.r1 Soares_feta	1.19e-01	205	20	0.3	371	41	AQ368917	HS_5021_B2_G09_SP6E RP	1.19e-01
133	20	0.3	321	36	AA093001	m1825.seq.F Human feta	1.19e-01	206	20	0.3	371	39	AQ212127	HS_3241_B1_G07_MR CIT	1.19e-01
134	21	0.3	324	35	AA027751	ml15b12.r1 Soares mous	6.31e-03	207	20	0.3	372	33	N97723	1151C3 czapFDD2.1, De	1.19e-01
135	20	0.3	324	37	B43947	HS-1058-B1-D01-MF.abi	1.19e-01	208	21	0.3	372	28	AI551615	ve37e07.y1 Soares mous	6.31e-03
136	21	0.3	325	39	AQ089851	HS_3001.A2_B02_MR CIT	6.31e-03	209	21	0.3	373	37	B40243	HS-1051-A1-G03-MF.abi	6.31e-03
137	21	0.3	328	25	AT000974	AT000974 Bombyx mandar	6.31e-03	210	21	0.3	374	25	FR0038621	AU038621 Dictyostelium	6.31e-03
138	20	0.3	330	32	H84763	ys70e02.r1 Soares reti	1.19e-01	211	21	0.3	374	37	FR0034383	Fugu rubripes GSS sequ	6.31e-03
139	20	0.3	330	24	AU034903	AU034903 Dictyostelium	1.19e-01	212	20	0.3	374	39	AQ084961	HS_2265_B2_E03_MF CIT	1.19e-01
140	20	0.3	334	20	AA855840	vw75e09.r1 Stratagene	1.19e-01	213	20	0.3	374	41	AQ356265	CITBI-El-2529D12.TR CI	1.19e-01
141	20	0.3	337	28	AI559913	th87d09.x1 Soares_NHMH	1.19e-01	214	20	0.3	374	39	AQ135849	HS_3064_A2_H06_MR CIT	1.19e-01
142	20	0.3	337	38	AQ047247	RPC111-36A1.TK RPC111	1.19e-01	215	20	0.3	377	15	C68758	C68758 Yuji Kohara unp	1.19e-01
143	22	0.3	338	9	AA163390	ms66b10.r1 Stratagene	2.90e-04	216	20	0.3	377	39	AQ103968	HS_3107_A1_D10_T7 CIT	1.19e-01
144	20	0.3	338	15	C75167	C75167 Human pancreati	1.19e-01	217	21	0.3	378	21	AI020787	ub04g04.r1 Soares mous	6.31e-03
145	20	0.3	338	32	H84778	ys71f05.s1 Soares reti	1.19e-01	218	20	0.3	378	40	AQ275485	RPC1-1-107N1Sp6 RPC1-1	1.19e-01
146	22	0.3	339	12	AA396639	vb29d09.r1 Soares mous	2.90e-04	219	20	0.3	379	27	AI470580	ti92a05.x1 NCI_CGAP_Ki	1.19e-01
147	21	0.3	339	25	AU038423	AU038423 Dictyostelium	6.31e-03	220	20	0.3	380	38	AQ061897	CIT-HSP-2357I14.TR CIT	1.19e-01
148	20	0.3	340	10	AA256396	zr85g04.s1 Soares_NHMH	1.19e-01	221	20	0.3	380	37	FR0019521	F.rubripes GSS sequenc	1.19e-01
149	20	0.3	340	37	FR0032336	YJ32f09.s1 Soares sequ	1.19e-01	222	20	0.3	380	23	AI146206	UI-R-El-fa-c-04-0-UI.s	1.19e-01
150	20	0.3	342	30	H01895	YJ32f09.s1 Soares plac	1.19e-01	223	21	0.3	381	18	AA797405	vw27e09.r1 Soares mous	6.31e-03
151	22	0.3	342	11	AA311800	EST182536 Jurkat T-cel	2.90e-04	224	20	0.3	382	31	R85019	yo40h06.r1 Soares adul	1.19e-01
152	22	0.3	345	21	AA959845	vw54h11.s1 Soares mous	2.90e-04	225	20	0.3	382	11	AA324362	EST27173 Cerebellum II	1.19e-01
153	21	0.3	345	33	N75835	za96b10.s1 Soares_feta	6.31e-03	226	20	0.3	383	36	AA114906	z104e10.s1 Soares_preg	1.19e-01
154	20	0.3	345	38	B85569	RPC111-20A16.TV RPC111	1.19e-01	227	20	0.3	383	39	AQ204831	HS_3230_B1_E11_MR CIT	1.19e-01
155	20	0.3	345	9	AA200899	mul6f11.r1 Soares 2NbM	1.19e-01	228	20	0.3	383	15	AA584948	nn41b09.s1 NCI_CGAP_GC	1.19e-01
156	20	0.3	345	32	H80030	ys65h10.s1 Soares reti	1.19e-01	229	20	0.3	384	22	AU018402	AU018402 Mouse eight-c	1.19e-01

522	21	0.3	528	9	AA176000	ms99d05.r1 Soares mous	6.31e-03	595	20	0.3	597	18	AA803101	GM06994.5prime GM Dros	1.19e-01
523	21	0.3	529	41	AQ283869	RPC111-78C19.TJ RPC111	6.31e-03	596	20	0.3	597	37	FR0012562	F.rubripes GSS sequenc	1.19e-01
524	21	0.3	530	26	AA818627	UI-R-A0-aw-b-03-0-UI.s	6.31e-03	597	20	0.3	599	37	FR0012566	F.rubripes GSS sequenc	1.19e-01
525	21	0.3	530	20	AA896171	vx62a07.r1 Stratagene	6.31e-03	598	20	0.3	602	37	FR0031775	Fugu rubripes GSS sequ	1.19e-01
526	20	0.3	530	28	AI562985	TENS2145 T. cruzi epim	1.19e-01	599	21	0.3	603	37	FR0026338	F.rubripes GSS sequenc	6.31e-03
527	20	0.3	533	38	B56766	CIT-HSP-2007M5.TPB CIT	1.19e-01	600	20	0.3	603	34	W72372	zdf2f07.s1 Soares.feta	1.19e-01
528	20	0.3	534	23	AI110047	GH09488.5prime GH Dros	1.19e-01	601	20	0.3	603	24	AI258156	LP01280.5prime LP Dros	1.19e-01
529	21	0.3	534	42	AQ405256	HS_5038_A1_B02_T7 RPCI	6.31e-03	602	21	0.3	605	37	B72806	RPC111-10F18.TP RPC111	6.31e-03
530	20	0.3	534	40	AQ265429	CITBI-EL-2509020.TF CI	1.19e-01	603	20	0.3	605	37	FR0023876	F.rubripes GSS sequenc	1.19e-01
531	20	0.3	536	37	FR0031160	Fugu rubripes GSS sequ	1.19e-01	604	21	0.3	606	37	AG008998	Homo sapiens genomic D	6.31e-03
532	20	0.3	538	28	AI541873	SD07826.5prime SD Dros	1.19e-01	605	20	0.3	606	37	AG008998	Homo sapiens genomic D	6.31e-03
533	22	0.3	538	15	AA1615307	vo01h05.r1 Stratagene	2.90e-04	606	20	0.3	606	37	AG008998	Homo sapiens genomic D	6.31e-03
534	21	0.3	541	27	AI426983	mn13b11.x1 Beddington	6.31e-03	607	21	0.3	608	41	AQ323864	RPC111-106J6.TJ RPC111	1.19e-01
535	20	0.3	542	41	AQ320052	RPC111-101F23.TV RPC11	1.19e-01	608	21	0.3	608	28	AI543170	SD09809.5prime SD Dros	6.31e-03
536	20	0.3	542	41	AQ342659	RPC111-112C19.TV RPC11	1.19e-01	609	20	0.3	609	41	AQ328359	nbxb0042N12f CUGI Rice	1.17e-05
537	20	0.3	544	38	B93396	CIT-HSP-2173B4.TR CIT-	1.19e-01	610	21	0.3	612	38	AQ061226	Fugu rubripes GSS sequ	1.19e-01
538	21	0.3	547	40	AQ248087	HS_2015_A1_G06_MR CIT	6.31e-03	611	20	0.3	612	38	B56278	CIT-HSP-2006I11.TR CIT	1.19e-01
539	20	0.3	548	20	AA898110	NCM3B9T7 Mycelial Neur	1.19e-01	612	20	0.3	614	41	AQ354096	CITBI-EL-2530G16.TR CI	1.19e-01
540	20	0.3	548	17	AA438832	LD13191.5prime LD Dros	1.19e-01	613	20	0.3	614	37	B63214	RPC111-1D2.TVB RPC111	1.19e-01
541	21	0.3	549	18	AA801162	EST190659 Normalized r	6.31e-03	614	20	0.3	614	37	FR0033208	Fugu rubripes GSS sequ	1.19e-01
542	21	0.3	550	42	AQ401887	HS_5046_B1_H03_T7 RPCI	6.31e-03	615	21	0.3	615	37	FR0018167	F.rubripes GSS sequenc	6.31e-03
543	20	0.3	550	20	AA908081	TENS0921 T. cruzi epim	1.19e-01	616	22	0.3	616	37	B18209	PBAC 2.34 re Mouse BAC	2.90e-04
544	20	0.3	551	28	AI510924	T7040 MVAT4 bloodstrea	1.19e-01	617	20	0.3	617	37	FR0003330	F.rubripes GSS sequenc	1.19e-01
545	24	0.3	552	41	AQ306865	HS_2196_B1_G09_MR CIT	4.19e-07	618	21	0.3	617	37	FR0034384	Fugu rubripes GSS sequ	6.31e-03
546	21	0.3	554	16	C76454	C76454 Mouse 3.5-dpc b	6.31e-03	619	21	0.3	617	37	FR0005249	F.rubripes GSS sequenc	6.31e-03
547	20	0.3	554	37	FR0029298	Fugu rubripes GSS sequ	1.19e-01	620	20	0.3	618	15	AA567321	HL01039.5prime HL Dros	1.19e-01
548	20	0.3	554	37	FR0027774	F.rubripes GSS sequenc	1.19e-01	621	20	0.3	618	37	FR0002429	F.rubripes GSS sequenc	1.19e-01
549	20	0.3	555	28	AI534169	SD06690.3prime SD Dros	1.19e-01	622	21	0.3	618	37	FR0020821	F.rubripes GSS sequenc	6.31e-03
550	21	0.3	558	25	AU038192	AU038192 Dictyostelium	6.31e-03	623	21	0.3	618	37	FR0030196	Fugu rubripes GSS sequ	6.31e-03
551	20	0.3	559	26	AI413460	me77c01.x1 Soares mous	1.19e-01	624	20	0.3	618	37	FR0033612	Fugu rubripes GSS sequ	1.19e-01
552	20	0.3	560	38	B53265	CIT-HSP-2009K7.TF CIT-	1.19e-01	625	20	0.3	618	37	FR0007983	F.rubripes GSS sequenc	1.19e-01
553	20	0.3	561	21	AA942935	EST198434 Normalized r	1.19e-01	626	20	0.3	618	37	FR0013834	F.rubripes GSS sequenc	1.19e-01
554	22	0.3	563	37	B03625	CSRL-183G4-u CSRL flow	2.90e-04	627	20	0.3	619	37	FR0002393	F.rubripes GSS sequenc	1.19e-01
555	20	0.3	564	37	FR0022187	F.rubripes GSS sequenc	1.19e-01	628	20	0.3	619	37	FR0003792	F.rubripes GSS sequenc	1.19e-01
556	20	0.3	567	42	AQ379945	RPC111-163H11.TJ RPC11	1.19e-01	629	22	0.3	619	37	FR0032711	Fugu rubripes GSS sequ	2.90e-04
557	20	0.3	568	37	FR0010102	F.rubripes GSS sequenc	1.19e-01	630	20	0.3	619	37	FR0008519	F.rubripes GSS sequenc	1.19e-01
558	20	0.3	568	39	AQ014272	RPC111-22H3.TKBF RPC11	1.19e-01	631	20	0.3	619	37	FR0003801	F.rubripes GSS sequenc	1.19e-01
559	20	0.3	569	25	AU040159	AU040159 Mouse four-ce	1.19e-01	632	20	0.3	619	37	FR0006470	F.rubripes GSS sequenc	1.19e-01
560	20	0.3	569	9	AA222121	my29g10.r1 Barstead mo	1.19e-01	633	20	0.3	623	39	AQ108802	CIT-HSP-2372G17.TR CIT	1.19e-01
561	20	0.3	569	42	FR0087566	RPC111-141B18.TV RPC11	1.19e-01	634	20	0.3	623	17	AA759928	vv32g11.r1 Stratagene	1.19e-01
562	21	0.3	571	40	AQ239499	CIT-HSP-2386N1.TF.1 CI	6.31e-03	635	21	0.3	624	37	AG011641	Homo sapiens genomic D	1.19e-01
563	20	0.3	572	42	AQ421867	RPCI-11-168C9.TJ RPCI-	1.19e-01	636	21	0.3	625	37	AG008999	CIT-HSP-2022E5.TF CIT-	1.17e-05
564	20	0.3	572	36	AA082619	zn41b08.r1 Stratagene	1.19e-01	637	23	0.3	625	38	B64278	Homo sapiens genomic D	1.19e-01
565	20	0.3	574	15	AA604994	no73f02.s1 NCI_CGAP_AA	1.19e-01	638	20	0.3	625	37	AG008999	Homo sapiens genomic D	1.19e-01
566	20	0.3	576	22	AI052139	oy30d08.x1 Soares_para	1.19e-01	639	20	0.3	626	14	AA539914	LD19214.5prime LD Dros	1.19e-01
567	20	0.3	576	20	AA919115	ol85g11.s1 NCI_CGAP_Ki	1.19e-01	640	20	0.3	626	37	AG012222	Homo sapiens genomic D	6.31e-03
568	20	0.3	576	42	AQ417346	RPCI-11-188E9.TV RPCI-	6.31e-03	641	21	0.3	629	37	AG009011	Homo sapiens genomic D	6.31e-03
569	21	0.3	576	18	AA760852	nz14f11.s1 NCI_CGAP_GC	1.19e-01	642	22	0.3	630	34	W67899	zd42a06.r1 Soares.feta	2.90e-04
570	20	0.3	577	39	AQ083665	CPG0564A CPIOAGDNA1 C	1.19e-01	643	21	0.3	632	38	AQ020815	CIT-HSP-2310H13.TR CIT	6.31e-03
571	20	0.3	578	42	AQ441833	HS_5106_B1_E01_T7A RPC	1.19e-01	644	20	0.3	632	24	AU033646	AU033646 Dictyostelium	1.19e-01
572	20	0.3	578	39	C78218	C78218 Mouse 3.5-dpc b	1.19e-01	645	20	0.3	632	28	AI534159	SD06678.5prime SD Dros	1.19e-01
573	20	0.3	579	16	C78218	LP04519.5prime LP Dros	1.19e-01	646	20	0.3	632	40	AQ243426	HS_2058_A2_G01_MR CIT	1.19e-01
574	20	0.3	579	24	AI260592	F.rubripes GSS sequenc	1.19e-01	647	20	0.3	633	17	AA735368	LD21193.5prime LD Dros	1.19e-01
575	20	0.3	581	37	FR0002742	CSRL-80a9-u CSRL flow	1.19e-01	648	21	0.3	634	20	C91198	C91198 Dictyostelium d	6.31e-03
576	20	0.3	583	37	B06412	F.rubripes GSS sequenc	1.19e-01	649	20	0.3	634	25	AI297857	LP12284.3prime LP Dros	1.19e-01
577	20	0.3	583	37	FR0021168	F.rubripes GSS sequenc	1.19e-01	650	20	0.3	635	39	AQ008908	RPC111-22K17.TVB RPC11	1.19e-01
578	21	0.3	583	20	C90163	C90163 Dictyostelium d	6.31e-03	651	20	0.3	635	37	AG008997	Homo sapiens genomic D	1.19e-01
579	20	0.3	584	24	AI222373	gg98a05.x1 Soares.NFL	1.19e-01	652	21	0.3	637	38	AQ075108	CIT-HSP-2353L5.TR CIT-	6.31e-03
580	20	0.3	584	41	AQ335355	HS_5016_B2_G12.SP6E RP	1.19e-01	653	20	0.3	638	41	AQ320770	RPC111-92E22.TV RPC111	1.19e-01
581	20	0.3	585	20	AA920306	vx93g09.r1 Soares 2NbM	1.19e-01	654	20	0.3	647	37	AG012221	Homo sapiens genomic D	1.19e-01
582	20	0.3	585	39	AQ202050	RPC111-45J14.TK RPC111	1.19e-01	655	20	0.3	647	41	AQ355933	CITBI-EL-2532A18.TF CI	1.19e-01
583	20	0.3	585	22	AU016721	AU016721 Mouse two-cel	1.19e-01	656	20	0.3	649	37	B71494	RPC111-8N9.TP RPC111 H	1.19e-01
584	21	0.3	586	37	FR0021323	F.rubripes GSS sequenc	6.31e-03	657	20	0.3	650	26	AU002712	AU002712 Bombyx mori p	1.19e-01
585	20	0.3	587	37	FR0024133	F.rubripes GSS sequenc	1.19e-01	658	20	0.3	650	37	AG014567	Homo sapiens genomic D	1.19e-01
586	21	0.3	587	41	AQ332027	HS_5002_B1_C09_T7 RPCI	6.31e-03	659	21	0.3	650	36	AA118174	mn13b11.r1 Beddington	6.31e-03
587	21	0.3	588	25	AI327289	mp56b11.x1 Soares 2NbM	6.31e-03	660	20	0.3	652	41	AQ283476	RPC111-79G11.TV RPC111	1.19e-01
588	20	0.3	588	42	AQ414581	RPCI-11-177C3.TJ RPCI-	1.19e-01	661	20	0.3	652	28	AI514955	LD46602.5prime LD Dros	1.19e-01
589	20	0.3	589	37	FR0011084	F.rubripes GSS sequenc	1.19e-01	662	21	0.3	654	37	AG015611	Homo sapiens genomic D	6.31e-03
590	20	0.3	591	24	AU033763	AU033763 Dictyostelium	1.19e-01	663	20	0.3	658	9	AA186034	mt35h02.r1 Soares mous	1.19e-01
591	20	0.3	592	37	B62733	T20K16TF.1 TAMU Arabid	1.19e-01	664	20	0.3	659	37	AG012244	Homo sapiens genomic D	1.19e-01
592	20	0.3	592	39	AQ201178	RPC111-46M8.TJ RPC111	1.19e-01	665	20	0.3	660	41	AQ347480	RPC111-12614.TJ RPC111	1.19e-01
593	20	0.3	593	32	N23817	yx36f12.r1 Soares mela	1.19e-01	666	21	0.3	661	41	AQ286662	RPC111-76B9.TJ RPC111	6.31e-03
594	20	0.3	594	38	AQ044107	CIT-HSP-2318P22.TF CIT	1.19e-01	667	20	0.3	663	24	AA803688	GM13983.5prime GM Dros	1.19e-01

C	668	23	0.3	664	41	AQ289098	nbxb0034M17f CUGI Rice	1.17e-05	741	19	0.2	271	40	AQ278873	CITBI-El-2523D18.TR CI	1.91e+00
C	669	20	0.3	669	39	AQ014227	RPCI11-22K17.TKBFC RPC	1.19e-01	742	19	0.2	278	41	AQ344015	RPCI11-124J9.TV RPCI11	1.91e+00
C	670	21	0.3	676	34	AA000678	mg35f01.r1 Soares mous	6.31e-03	743	19	0.2	279	9	AA168740	ms34a02.r1 Stratagene	1.91e+00
C	671	20	0.3	676	26	AU002893	AU002893 Bombyx mori p	1.19e-01	744	19	0.2	279	40	AQ268218	RPCI11-73L8.TJ RPCI11	1.91e+00
C	672	22	0.3	677	42	AQ25634	CITBI-El-2556B7.TF CIT	2.90e-04	745	19	0.2	288	28	AI508764	VC21f11.y1 Ko mouse em	1.91e+00
C	673	23	0.3	679	17	AA697360	HL02318.5prime HL Dros	1.17e-05	746	19	0.2	289	15	AA606720	vo07c04.r1 Stratagene	1.91e+00
C	674	20	0.3	679	42	AQ415324	RPCI-11-165D17.TJ RPCI	1.19e-01	747	19	0.2	292	28	AI508769	vc22b03.y1 Ko mouse em	1.91e+00
C	675	20	0.3	679	33	W02556	za49h01.r1 Soares feta	1.19e-01	748	19	0.2	293	25	AA680741	LmFrAm0250 Leishmania	1.91e+00
C	676	20	0.3	685	42	AQ417081	RPCI-11-177K16.TV RPCI	1.19e-01	749	19	0.2	293	36	AA078367	7P02D11 Chromosome 7 P	1.91e+00
C	677	20	0.3	687	37	AG007660	Homo sapiens genomic D	1.19e-01	750	19	0.2	295	16	AA675476	vr72d01.s1 Knowles Sol	1.91e+00
C	678	20	0.3	689	24	AU034828	AU034828 Dictyostelium	1.19e-01	751	19	0.2	299	9	AA167157	zp06f03.r1 Stratagene	1.91e+00
C	679	21	0.3	689	17	AA754976	vu55g05.r1 Soares mous	6.31e-03	752	19	0.2	304	20	AA907379	ok95e02.s1 NCI_CGAP_Lu	1.91e+00
C	680	20	0.3	691	37	AG007659	Homo sapiens genomic D	1.19e-01	753	19	0.2	308	11	AA334945	EST39226 Embryo, 9 wee	1.91e+00
C	681	20	0.3	696	37	AG007658	Homo sapiens genomic D	1.19e-01	754	19	0.2	309	31	H27701	Y161c12.r1 Soares brea	1.91e+00
C	682	20	0.3	698	40	AQ026380	CITBI-El-2503H5.TF CIT	1.19e-01	755	19	0.2	309	37	FR0004818	F.rubripes GSS sequenc	1.91e+00
C	683	20	0.3	702	25	AU039558	AU039558 Dictyostelium	1.19e-01	756	19	0.2	310	37	FR0029693	Fugu rubripes GSS sequ	1.91e+00
C	684	20	0.3	708	24	AU034494	AU034494 Dictyostelium	1.19e-01	757	19	0.2	315	20	AA863841	vx09f06.r1 Soares 2NbM	1.91e+00
C	685	20	0.3	709	24	AU033788	AU033788 Dictyostelium	1.19e-01	758	19	0.2	322	36	AA117147	mo62d04.r1 Stratagene	1.91e+00
C	686	21	0.3	710	18	AA798410	vy06e08.r1 Stratagene	6.31e-03	759	19	0.2	324	39	AQ084946	HS_2265_B2_C10_MF CIT	1.91e+00
C	687	20	0.3	713	21	AA981409	ug99c05.r1 Soares mous	1.19e-01	760	19	0.2	326	27	AI457887	tj48a01.x1 Soares_NSF_	1.91e+00
C	688	21	0.3	718	38	AQ079291	CIT-HSP-2365K18.TR CIT	6.31e-03	761	19	0.2	328	26	AI387168	GH17619.5prime GH Dros	1.91e+00
C	689	20	0.3	719	41	AQ362378	nbxb0049P21r CUGI Rice	1.19e-01	762	19	0.2	329	25	AU046128	AU046128 Mouse sixteen	1.91e+00
C	690	20	0.3	721	24	AU033551	AU033551 Dictyostelium	1.19e-01	763	19	0.2	329	13	AA409995	EST01811 Mouse 7.5 dpc	1.91e+00
C	691	20	0.3	723	24	AU033533	AU033533 Dictyostelium	1.19e-01	764	19	0.2	329	35	AA058418	zk81e01.r1 Soares_preg	1.91e+00
C	692	20	0.3	723	37	AG001964	Homo sapiens genomic D	1.19e-01	765	19	0.2	331	39	AQ086321	HS_2166_B1_F06_MF CIT	1.91e+00
C	693	20	0.3	724	37	AG009112	Homo sapiens genomic D	1.19e-01	766	19	0.2	335	28	AI506626	vn47e04.x1 Barstead mo	1.91e+00
C	694	20	0.3	729	37	AG009113	Homo sapiens genomic D	1.19e-01	767	19	0.2	335	15	AA582524	nn50e06.s1 NCI_CGAP_Ki	1.91e+00
C	695	21	0.3	740	20	C84093	C84093 Dictyostelium d	6.31e-03	768	19	0.2	345	38	AQ004401	CIT-HSP-2295L19.TR CIT	1.91e+00
C	696	20	0.3	740	40	AQ269380	HS_2007_Al_G03_T7 CIT	1.19e-01	769	19	0.2	345	25	AI289936	qv02h10.x1 NCI_CGAP_Ki	1.91e+00
C	697	20	0.3	752	21	AA951110	LD31410.5prime LD Dros	1.19e-01	770	19	0.2	346	17	AA717368	vp42g10.r1 Barstead mo	1.91e+00
C	698	20	0.3	754	40	AQ273724	nbxb0030D18r CUGI Rice	1.19e-01	771	19	0.2	346	28	AI567063	tp49g02.x1 NCI_CGAP_Ut	1.91e+00
C	699	20	0.3	760	27	AI477982	fb49h08.x1 Zebrafish W	1.19e-01	772	19	0.2	348	24	AA680796	LmFrAm0333 Leishmania	1.91e+00
C	700	21	0.3	782	25	AI327282	mo62h06.x1 Stratagene	6.31e-03	773	19	0.2	351	36	AA137632	mq99d03.r1 Soares mous	1.91e+00
C	701	20	0.3	786	24	AU033453	AU033453 Dictyostelium	1.19e-01	774	19	0.2	351	37	FR0009367	F.rubripes GSS sequenc	1.91e+00
C	702	20	0.3	813	24	AU033632	AU033632 Dictyostelium	1.19e-01	775	19	0.2	351	40	AQ165716	HS_3065_B1_F09_MR CIT	1.91e+00
C	703	20	0.3	818	15	AA608727	ae56e09.s1 Stratagene	1.19e-01	776	19	0.2	352	29	AI568849	to23a10.x1 NCI_CGAP_Ut	1.91e+00
C	704	20	0.3	820	42	AQ050492	nbxb0004F05r CUGI Ric	1.19e-01	777	19	0.2	353	9	AA166094	ms23e07.r1 Stratagene	1.91e+00
C	705	21	0.3	823	25	AI323807	mm74b12.x1 Stratagene	6.31e-03	778	19	0.2	355	41	AQ356090	CITBI-El-2529B20.TR CI	1.91e+00
C	706	20	0.3	855	17	AA697762	HL03118.5prime HL Dros	1.19e-01	779	19	0.2	356	16	AA673751	vs64e06.r1 Stratagene	1.91e+00
C	707	20	0.3	880	37	B13213	F22F23-Sp6 IGF ArabidG	1.19e-01	780	19	0.2	359	42	AQ385862	RPCI11-142M22.TJ RPCI1	1.91e+00
C	708	21	0.3	912	37	B12653	F26G16-T7 IGF Arabidop	6.31e-03	781	19	0.2	360	20	AA907053	om10g07.s1 Soares_NFL_	1.91e+00
C	709	21	0.3	915	37	B13200	T19M22-T7 TAMU Arabido	6.31e-03	782	19	0.2	361	9	AA221362	mwl1h07.r1 Soares mous	1.91e+00
C	710	22	0.3	934	18	AA769056	oa74a11.s1 NCI_CGAP_GC	2.90e-04	783	19	0.2	362	22	AU023132	AU023132 Mouse unferti	1.91e+00
C	711	20	0.3	980	39	AF010974	Homo sapiens chromosom	1.19e-01	784	19	0.2	364	31	H65043	yr69b11.r1 Soares feta	1.91e+00
C	712	20	0.3	1064	22	AI068630	mgae0003CD05f Magnapor	1.19e-01	785	19	0.2	365	28	AI551793	vo44h12.x1 Barstead mo	1.91e+00
C	713	21	0.3	1120	37	B11801	T4M23-Sp6 TAMU Arabido	6.31e-03	786	19	0.2	366	33	N72930	vv47f09.r1 Soares feta	1.91e+00
C	714	20	0.3	1189	38	AQ034099	l(3)j8C8 Drosophila me	1.19e-01	787	19	0.2	366	31	H32652	EST107948 Rat PC-12 ce	1.91e+00
C	715	20	0.3	1234	20	AF012875	AF012875 Bovine fetal	1.19e-01	788	19	0.2	367	26	AI415308	mc02f08.x1 Soares mous	1.91e+00
C	716	23	0.3	1577	23	AF083305	AF083305 Drosophila me	1.17e-05	789	19	0.2	369	12	AQ088386	HS_3000_A2_F01_MR CIT	1.91e+00
C	717	21	0.3	1801	42	AF101710	Homo sapiens chromosom	6.31e-03	790	19	0.2	369	19	AA365428	EST76462 Pineal gland	1.91e+00
C	718	21	0.3	6921	41	AF101618	Homo sapiens chromosom	6.31e-03	791	19	0.2	370	19	R00591	ye74b01.r1 Soares feta	1.91e+00
C	719	19	0.2	105	37	FR0022757	F.rubripes GSS sequenc	1.91e+00	792	19	0.2	371	8	D27614	CELK015D5R Yuji Kohara	1.91e+00
C	720	19	0.2	121	18	AA834402	of67h01.s1 NCI_CGAP_Co	1.91e+00	793	19	0.2	371	22	AI066711	oz87g01.x1 Soares_sene	1.91e+00
C	721	19	0.2	130	17	AA717013	vu61c10.r1 Soares mous	1.91e+00	794	19	0.2	372	38	AQ025890	l(2)k09217 Drosophila	1.91e+00
C	722	19	0.2	146	38	B82384	RPCI11-15C2.TPB RPCI11	1.91e+00	795	19	0.2	372	22	AI034673	LmLv39p10/413D Leishma	1.91e+00
C	723	19	0.2	148	40	AQ267084	RPCI11-72L4.TJ RPCI11	1.91e+00	796	19	0.2	377	27	AI449734	mr67a02.x1 Stratagene	1.91e+00
C	724	19	0.2	169	22	AI066368	TENU2484 T. cruzi epim	1.91e+00	797	19	0.2	377	26	AI359133	qy26a01.x1 NCI_CGAP_Br	1.91e+00
C	725	19	0.2	176	9	AA180556	MBAFCF702T3 Brugia ma	1.91e+00	798	19	0.2	378	38	AQ065235	HS_2263_A2_MF_E02 CIT	1.91e+00
C	726	19	0.2	180	33	N73077	za08c02.s1 Soares mela	1.91e+00	799	19	0.2	379	18	AA773548	ab57h10.s1 Stratagene	1.91e+00
C	727	19	0.2	207	8	T40481	ya02d01.s2 Stratagene	1.91e+00	800	19	0.2	380	27	AI467078	vd09g10.x1 Knowles Sol	1.91e+00
C	728	19	0.2	216	10	AA250810	zs06a03.s1 NCI_CGAP_GC	1.91e+00	801	19	0.2	381	39	AQ122959	HS_3094_B1_H01_MR CIT	1.91e+00
C	729	19	0.2	222	38	AQ003150	CIT-HSP-2204A20.TR CIT	1.91e+00	802	19	0.2	381	40	AQ166244	HS_3076_B1_D02_MR CIT	1.91e+00
C	730	19	0.2	231	23	AI175697	EST219258 Normalized r	1.91e+00	803	19	0.2	382	16	AA617185	vj79a01.r1 Knowles Sol	1.91e+00
C	731	19	0.2	234	19	T86625	yd81a03.r1 Soares feta	1.91e+00	804	19	0.2	383	26	AI357484	qu01g06.x1 NCI_CGAP_Co	1.91e+00
C	732	19	0.2	237	38	AQ066938	HS_2228_Al_B10_MF CIT	1.91e+00	805	19	0.2	383	15	AA571266	vl90e10.r1 Stratagene	1.91e+00
C	733	19	0.2	239	19	T66910	ya50f11.s1 Soares feta	1.91e+00	806	19	0.2	386	17	AA730643	nw42h12.s1 NCI_CGAP_Ew	1.91e+00
C	734	19	0.2	242	42	AQ385105	RPCI11-152D6.TJ RPCI11	1.91e+00	807	19	0.2	387	39	AQ118356	HS_3004_Al_F11_MR CIT	1.91e+00
C	735	19	0.2	248	28	AI536307	ma84h09.y1 Soares mous	1.91e+00	808	19	0.2	388	20	AA890534	ak11b11.s1 Soares_para	1.91e+00
C	736	19	0.2	250	14	AA498860	vi82h07.r1 Stratagene	1.91e+00	809	19	0.2	389	15	AA575448	vl90b01.r1 Stratagene	1.91e+00
C	737	19	0.2	252	17	AA747581	nx92d12.s1 NCI_CGAP_GC	1.91e+00	810	19	0.2	390	19	R23476	yh39e04.r1 Soares plac	1.91e+00
C	738	19	0.2	261	8	T17109	NIB340 Normalized infn	1.91e+00	811	19	0.2	392	41	AQ301018	HS_3105_A2_H01_MR CIT	1.91e+00
C	739	19	0.2	262	38	B93088	CIT-HSP-2173J15.TF CIT	1.91e+00	812	19	0.2	394	13	AA414554	vc60f11.s1 Knowles Sol	1.91e+00
C	740	19	0.2	270	14	AA525815	ni61c05.s1 NCI_CGAP_Ov	1.91e+00	813	19	0.2	395	27	AA957628		

814	19	0.2	401 27	AI452354	mq88a04.x1 Stratagene	1.91e+00	887	19	0.2	480 32	H71462	yu71b05.s1 Weizmann Ol	1.91e+00
815	19	0.2	401 42	AQ445401	GSSTc01195 Trypanosoma	1.91e+00	888	19	0.2	481 21	AA993885	ou02h09.s1 Soares_tota	1.91e+00
816	19	0.2	404 38	AQ039804	CIT-HSP-2323K24.TF CIT	1.91e+00	889	19	0.2	487 21	AI015955	ov30a10.x1 Soares_test	1.91e+00
817	19	0.2	406 16	AA646074	vn03c04.r1 Stratagene	1.91e+00	890	19	0.2	489 42	AQ444673	GSSTc01932 Trypanosoma	1.91e+00
818	19	0.2	408 17	AA158769	zo03h06.s1 Stratagene	1.91e+00	891	19	0.2	490 41	AQ354677	CITBI-E1-2538A4.TF CIT	1.91e+00
819	19	0.2	408 19	AA726533	vu92h10.r1 Stratagene	1.91e+00	892	19	0.2	493 17	AA714930	nv49c05.r1 NCI_CGAP_Ew	1.91e+00
820	19	0.2	408 19	T98528	ye70b09.r1 Soares feta	1.91e+00	893	19	0.2	494 27	AA957703	UI-R-E1-fw-g-10-0-UI.s	1.91e+00
821	19	0.2	413 25	AU043874	AU043874 Mouse sixteen	1.91e+00	894	19	0.2	495 26	AA956887	UI-R-E1-fr-a-06-0-UI.s	1.91e+00
822	19	0.2	413 17	AA693962	zi53e02.s1 Soares_feta	1.91e+00	895	19	0.2	495 38	B50693	CIT-HSP-581010.TP CIT-	1.91e+00
823	19	0.2	413 17	AA693962	NIB357 Normalized inf	1.91e+00	896	19	0.2	501 25	AI330436	fa92f10.x1 zebrafish f	1.91e+00
824	19	0.2	414 39	AQ131155	HS_3036_A1_G05_MR CIT	1.91e+00	897	19	0.2	501 40	AQ267939	RPCI11-72K14.TK RPCI11	1.91e+00
825	19	0.2	414 37	B44934	HS_1060-A2-C12-MF.abi	1.91e+00	898	19	0.2	501 28	AI546767	BSBML3SZ12G20SK Brugia	1.91e+00
826	19	0.2	414 28	AI545075	fb70d06.y1 zebrafish w	1.91e+00	899	19	0.2	504 31	H29383	ym32h03.r1 Soares inf	1.91e+00
827	19	0.2	415 30	H03010	YJ50f03.r1 Soares plac	1.91e+00	900	19	0.2	505 40	AQ190318	HS_3223_A1_G11_T7 CIT	1.91e+00
828	19	0.2	420 42	AQ443292	HS_5050_A2_H10_SP6E RP	1.91e+00	901	19	0.2	505 40	AQ182989	HS_3123_B1_B02_T7 CIT	1.91e+00
829	19	0.2	420 13	AA453131	zx38f04.r1 Soares_tota	1.91e+00	902	19	0.2	506 20	AA862021	oi46d04.s1 NCI_CGAP_HN	1.91e+00
830	19	0.2	421 26	AI384699	fb08b08.x1 zebrafish f	1.91e+00	903	19	0.2	507 28	AI505229	vg76a03.x1 Knowles Sol	1.91e+00
831	19	0.2	422 21	AI008726	EST203177 Normalized r	1.91e+00	904	19	0.2	509 41	AQ341248	RPCI11-120B24.TJ RPCI1	1.91e+00
832	19	0.2	424 21	AQ336272	HS_5019_B1_D10_SP6E RP	1.91e+00	905	19	0.2	512 8	T03771	IB877 Infant brain, Be	1.91e+00
833	19	0.2	425 20	AA892792	EST196595 Normalized r	1.91e+00	906	19	0.2	513 42	AQ426297	CITBI-E1-2563C20.TR CI	1.91e+00
834	19	0.2	427 39	AQ109795	CIT-HSP-2378K9.TF CIT-	1.91e+00	907	19	0.2	514 16	AA677682	zj72f10.s1 Soares_feta	1.91e+00
835	19	0.2	428 39	AQ222983	HS_2017_A2_D03_T7 CIT	1.91e+00	908	19	0.2	516 18	AA778401	zf35g12.s1 Soares_feta	1.91e+00
836	19	0.2	428 18	AA797134	vn43f03.r1 Stratagene	1.91e+00	909	19	0.2	516 41	AQ347929	RPCI11-105I6.TV RPCI11	1.91e+00
837	19	0.2	429 36	AA085388	zn07c05.s1 Stratagene	1.91e+00	910	19	0.2	517 37	FR0022225	F.rubripes GSS sequenc	1.91e+00
838	19	0.2	429 28	AI558652	fb68h05.y1 zebrafish w	1.91e+00	911	19	0.2	521 42	AQ444655	GSSTc01913 Trypanosoma	1.91e+00
839	19	0.2	431 27	AI428447	mo20b01.x1 Life Tech m	1.91e+00	912	19	0.2	523 14	AA528455	ne84f05.s1 NCI_CGAP_Ew	1.91e+00
840	19	0.2	432 18	AA768786	ocl7g05.s1 NCI_CGAP_GC	1.91e+00	913	19	0.2	524 41	AQ358692	HS_5029_A2_B06_T7 RPCI	1.91e+00
841	19	0.2	433 42	AQ443120	HS_5130_A1_A03_SP6E RP	1.91e+00	914	19	0.2	527 41	AQ356331	CITBI-E1-2536B12.TF CI	1.91e+00
842	19	0.2	434 42	AQ443371	HS_2231_B2_H12_MF CIT	1.91e+00	915	19	0.2	527 40	AQ189618	HS_3219_B1_G06_T7 CIT	1.91e+00
843	19	0.2	434 41	AQ333759	HS_5019_A2_B09_SP6E RP	1.91e+00	916	19	0.2	528 41	AQ322497	RPCI11-99C12.TJ RPCI11	1.91e+00
844	19	0.2	434 27	AI450873	ms01h09.x1 Stratagene	1.91e+00	917	19	0.2	528 20	AA892868	EST196671 Normalized r	1.91e+00
845	19	0.2	435 32	N34514	yy55b03.s1 Soares_mult	1.91e+00	918	19	0.2	530 39	AQ118624	HS_3019_B1_C11_T7 CIT	1.91e+00
846	19	0.2	436 27	AI471654	tl19a06.x1 NCI_CGAP_Co	1.91e+00	919	19	0.2	530 21	AA943550	EST199049 Normalized r	1.91e+00
847	19	0.2	437 36	AA139861	mq95b01.r1 Stratagene	1.91e+00	920	19	0.2	531 41	AQ322899	RPCI11-111K16.TJ RPCI1	1.91e+00
848	19	0.2	438 37	FR0015956	F.rubripes GSS sequenc	1.91e+00	921	19	0.2	531 39	AQ206538	HS_3234_A2_F01_T7 CIT	1.91e+00
849	19	0.2	438 38	AQ041227	CIT-HSP-2338H17.TF CIT	1.91e+00	922	19	0.2	533 41	AQ314055	RPCI11-104P5.TJ RPCI11	1.91e+00
850	19	0.2	439 28	AI506005	vl24f02.x1 Stratagene	1.91e+00	923	19	0.2	542 35	C06380	C06380 Human pancreati	1.91e+00
851	19	0.2	440 8	T48875	yb05h08.r1 Stratagene	1.91e+00	924	19	0.2	544 38	AQ008537	CIT-HSP-2283F22.TRB CI	1.91e+00
852	19	0.2	442 21	AI021889	ow96a05.x1 Soares_feta	1.91e+00	925	19	0.2	548 37	B72527	RPCI11-9E12.TV RPCI11	1.91e+00
853	19	0.2	444 33	N62273	yz89d12.s1 Soares_mult	1.91e+00	926	19	0.2	550 38	B94288	CIT-HSP-2166L11.TF CIT	1.91e+00
854	19	0.2	446 15	AA605872	fa20g08.s1 Ekkerearly	1.91e+00	927	19	0.2	557 41	AQ357255	CITBI-E1-2534P6.TR CIT	1.91e+00
855	19	0.2	447 31	H41204	yn88f12.r1 Soares adul	1.91e+00	928	19	0.2	560 37	FR0033997	Fugu rubripes GSS sequ	1.91e+00
856	19	0.2	448 34	W37349	zc09b12.s1 Soares_para	1.91e+00	929	19	0.2	562 22	AI034990	TENG0050 T. cruzi epim	1.91e+00
857	19	0.2	449 22	AI042756	uc75c04.x1 Sugano mous	1.91e+00	930	19	0.2	562 39	AQ003316	RPCI11-20D6.TPB RPCI11	1.91e+00
858	19	0.2	450 35	AA050579	my16e10.r1 Soares mous	1.91e+00	931	19	0.2	566 42	AQ425164	CITBI-E1-2561F9.TF CIT	1.91e+00
859	19	0.2	451 32	N30929	je54b05.r1 Soares feta	1.91e+00	932	19	0.2	568 9	AA152939	mr16b07.r1 Soares mous	1.91e+00
860	19	0.2	452 42	AQ390027	yx50d03.r1 Soares mela	1.91e+00	933	19	0.2	571 26	AI388902	GH19936.5prime GH Dros	1.91e+00
861	19	0.2	452 40	AA269904	RPCI11-158023.TV RPCI1	1.91e+00	934	19	0.2	571 41	AQ334270	HS_5005_A2_E11_T7 RPCI	1.91e+00
862	19	0.2	455 18	AQ015629	vit60e12.r1 Soares mous	1.91e+00	935	19	0.2	572 36	AA120692	mp72g10.r1 Soares 2NbM	1.91e+00
863	19	0.2	457 17	AA739114	CIT-HSP-2309N17.TR CIT	1.91e+00	936	19	0.2	581 8	T48132	yb25b11.s1 Stratagene	1.91e+00
864	19	0.2	457 18	AA739114	vv66f05.r1 Stratagene	1.91e+00	937	19	0.2	585 37	B72188	RPCI11-7K22.TP RPCI11	1.91e+00
865	19	0.2	459 15	AA596343	vo30b11.r1 Barstead mo	1.91e+00	938	19	0.2	588 16	C81242	C81242 Mouse 3.5-dpc b	1.91e+00
866	19	0.2	459 9	AA172697	ms19b08.r1 Stratagene	1.91e+00	939	19	0.2	589 37	FR0008663	F.rubripes GSS sequenc	1.91e+00
867	19	0.2	459 16	AA646320	vn12a02.r1 Stratagene	1.91e+00	940	19	0.2	590 18	C87122	C87122 Mouse fertilize	1.91e+00
868	19	0.2	460 13	AA475029	vh03g01.r1 Soares mous	1.91e+00	941	19	0.2	593 40	AQ266909	RPCI11-74N5.TJ RPCI11	1.91e+00
869	19	0.2	461 21	AI010917	EST205368 Normalized r	1.91e+00	942	19	0.2	594 37	FR0033784	Fugu rubripes GSS sequ	1.91e+00
870	19	0.2	464 22	AI035156	TENG0247 T. cruzi epim	1.91e+00	943	19	0.2	596 26	AI387954	GH18664.5prime GH Dros	1.91e+00
871	19	0.2	465 12	AA387138	vc22b03.r1 Ko mouse em	1.91e+00	944	19	0.2	597 38	AQ039681	CIT-HSP-2327G17.TR CIT	1.91e+00
872	19	0.2	467 37	B16425	342D12.TVB CIT978SKA1	1.91e+00	945	19	0.2	597 38	AQ061567	CIT-HSP-2348K13.TF CIT	1.91e+00
873	19	0.2	468 21	AI018216	ou16c01.x1 Soares_NFL	1.91e+00	946	19	0.2	597 37	FR0011107	F.rubripes GSS sequenc	1.91e+00
874	19	0.2	468 37	B36396	HS-1040-B2-A03-MF.abi	1.91e+00	947	19	0.2	601 9	AA210244	mo84h07.r1 Beddington	1.91e+00
875	19	0.2	468 37	B34315	HS-1024-B1-B05-MR.abi	1.91e+00	948	19	0.2	601 42	AQ380684	RPCI11-166O24.TJ RPCI1	1.91e+00
876	19	0.2	468 15	AA591808	vi49b11.r1 Beddington	1.91e+00	949	19	0.2	602 38	B59606	CIT-HSP-342K15.TPB CIT	1.91e+00
877	19	0.2	470 39	AQ232719	HS_2012_A2_H07_T7 CIT	1.91e+00	950	19	0.2	604 35	AA034011	zi06c10.r1 Soares_feta	1.91e+00
878	19	0.2	470 9	AA172873	ms20d02.r1 Stratagene	1.91e+00	951	19	0.2	605 40	AQ266522	RPCI11-75A2.TJ RPCI11	1.91e+00
879	19	0.2	475 25	AI334310	qq25g12.x1 Soares_NhM	1.91e+00	952	19	0.2	607 42	AQ394562	CITBI-E1-2553M14.TF CI	1.91e+00
880	19	0.2	475 21	AI004186	ou56d10.x1 NCI_CGAP_Br	1.91e+00	953	19	0.2	610 35	AA034012	zi06c10.s1 Soares_feta	1.91e+00
881	19	0.2	478 24	AI205185	ap13c07.x1 Schiller Ol	1.91e+00	954	19	0.2	617 39	AQ208264	HS_3219_A1_C06_T7 CIT	1.91e+00
882	19	0.2	478 32	N24387	yx14f02.r1 Soares mela	1.91e+00	955	19	0.2	618 40	AQ265832	CITBI-E1-2503L11.TR CI	1.91e+00
883	19	0.2	478 33	N67876	yz52b01.s1 Morton Feta	1.91e+00	956	19	0.2	618 37	FR0002343	F.rubripes GSS sequenc	1.91e+00
884	19	0.2	479 40	AQ186282	HS_3083_B2_H03_MF CIT	1.91e+00	957	19	0.2	618 37	FR0004638	F.rubripes GSS sequenc	1.91e+00
885	19	0.2	479 37	AF017579	Homo sapiens YAC 307A1	1.91e+00	958	19	0.2	619 37	FR0005223	F.rubripes GSS sequenc	1.91e+00
886	19	0.2	479 36	AA109538	mm01h03.r1 Stratagene	1.91e+00	959	19	0.2	619 37	FR0032807	Fugu rubripes GSS sequ	1.91e+00

Query Match 2.6%; Score 198; DB 32; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 TAAATCGAAATCAAAATCGTACTCTGACTACGGGTACGTAGAGAGGTCAACCATCAGCCG 61
|||||
Qy 2169 TAAATCGAAATCAAAATCGTACTCTGACTACGGGTACGTAGAGAGGTCAACCATCAGCCG 2228
|||||

Db 62 AAGATGATCGGTCAAGATAGAGAGGCTTGCTAGAGAGGAACATTATGATGTTCTCTAGT 121
|||||
Qy 2229 AAGATGATCGGTCAAGATAGAGAGGCTTGCTAGAGAGGAACATTATGATGTTCTCTAGT 2288
|||||

Db 122 CATCTAAAGTCGATGAAATTCGAAAGTTCTCATCGCAAACAAAGTGTGAATAGTGAT 181
|||||
Qy 2289 CATCTAAAGTCGATGAAATTCGAAAGTTCTCATCGCAAACAAAGTGTGAATAGTGAT 2348
|||||

Db 182 AATGGAGATATGATTAAT 199
|||||
Qy 2349 AATGGAGATATGATTAAT 2366
|||||

RESULT 3
LOCUS C39290 360 bp mRNA EST 10-SEP-1997
DEFINITION C39290 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
clone yk198f10 5', mRNA sequence.
ACCESSION C39290
NID 92375527
VERSION C39290.1 GI:2375527
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1393644.

Contact: Yuji Kohara
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Tel: 0559-75-0771
Fax: 0559-75-6240
Email: ykohara@dbj.nig.ac.j.
Location/Qualifiers
1. .360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk198f10"
/clone_lib="Yuji Kohara unpublished cDNA"

BASE COUNT 102 a 67 c 100 g 91 t
ORIGIN

Query Match 2.3%; Score 177; DB 15; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CTCTGACTACGGGTCAAGTACGAGAGGTCAACCATCAGCCGAGATGATCGGTCAAGATAGA 60
|||||
Qy 2190 CTCTGACTACGGGTCAAGTACGAGAGGTCAACCATCAGCCGAGATGATCGGTCAAGATAGA 2249
|||||

Db 61 AGGAGCTTCTAGAGAGGAACATTATGATGTTCTCTAGTCTATCTCTAAAGTCGATGAAATT 120
|||||
Qy 2250 AGGAGCTTCTAGAGAGGAACATTATGATGTTCTCTAGTCTATCTCTAAAGTCGATGAAATT 2309
|||||

Db 121 CTCGAAGTTCTCATCGCAAACAAAGTGTGAATAGTGATATGAGATATGATTAAT 177
|||||

Qy 2310 CTCGAAGTTCTCATCGCAAACAAAGTGTGAATAGTGATATGAGATATGATTAAT 2366
|||||

RESULT 4
LOCUS C51090 377 bp mRNA EST 11-SEP-1997
DEFINITION C51090 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
clone yk491a5 5', mRNA sequence.
ACCESSION C51090
NID 92388343
VERSION C51090.1 GI:2388343
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 377)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1405104.

Contact: Yuji Kohara
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Location/Qualifiers
1. .377
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/map="11q23"
/clone="yk491a5"
/clone_lib="Yuji Kohara unpublished cDNA"

BASE COUNT 106 a 74 c 103 g 92 t
ORIGIN

Query Match 2.0%; Score 153; DB 15; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.03e-296;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 GTC AACCATCAGCCG AAGATGATGATCGTCAAGATAGAGGAGCTTGCTAGAGAGGAACATT 76
|||||
Qy 2214 GTC AACCATCAGCCG AAGATGATGATCGTCAAGATAGAGGAGCTTGCTAGAGAGGAACATT 2273
|||||

Db 77 ATGATGTTCTCTAGTCATCTCTAAAGTCGATGAAATTCGGAAGTTCTCATCGCAAACAA 136
|||||
Qy 2274 ATGATGTTCTCTAGTCATCTCTAAAGTCGATGAAATTCGGAAGTTCTCATCGCAAACAA 2333
|||||

Db 137 GTGTTGAATAGTGATAATGAGATATGATTAAT 169
|||||
Qy 2334 GTGTTGAATAGTGATAATGAGATATGATTAAT 2366
|||||

RESULT 5
LOCUS C29898 300 bp mRNA EST 09-SEP-1997
DEFINITION C29898 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
clone yk228a6 3', mRNA sequence.
ACCESSION C29898
NID 92361694
VERSION C29898.1 GI:2361694
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 300)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,

TITLE Sano,M., Miyata,A. and Nishigaki,A.
JOURNAL Expression map of the C.elegans genome
COMMENT Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1393504.

Contact: Yuji Kohara
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FEATURES

source
1. .300
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk228a6"
/clone_lib="Yuji Kohara unpublished cDNA"
111 a 42 c 60 g 86 t 1 others

BASE COUNT

Query Match 0.4%; Score 29; DB 15; Length 300;
Best Local Similarity 96.7%; Pred. No. 5.37e-15;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 171 TACTGTANTTTTCGCTACGAGATATTTTC 200
||||| ||||| ||||| ||||| ||||| |||||
Cp 1423 TACTGTAGTTTTCGCTACGAGATATTTTC 1394

RESULT 6

LOCUS D64660 337 bp mRNA EST 13-DEC-1995
DEFINITION CELK086DZR Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk86d12 3', mRNA sequence.

ACCESSION

NID g1116350

VERSION D64660.1 GI:1116350

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 337)

REFERENCE Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and

AUTHORS Tabara,H.

TITLE Toward an expression map of the C.elegans genome

JOURNAL Unpublished (1994)

COMMENT On Apr 14, 1993 this sequence version replaced gi:503294.

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High quality sequence stop: 267.

Location/Qualifiers

FEATURES

source

1. .337

/organism="Caenorhabditis elegans"

/strain="CB1489 him-8(e1489)"

/note="dev_stage=varied, sex=Hermaphrodite male,

tissue_type=whole animal"

/db_xref="taxon:6239"

/map="17"

/clone="yk86d12"

/clone_lib="Yuji Kohara unpublished cDNA"

116 a 52 c 72 g 94 t 3 others

BASE COUNT

ORIGIN

Query Match 0.4%; Score 29; DB 32; Length 337;
Best Local Similarity 100.0%; Pred. No. 5.37e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 178 TACTGTAGTTTTCGCTACGAGATATTTTG 206
||||| ||||| ||||| ||||| ||||| |||||
Cp 1423 TACTGTAGTTTTCGCTACGAGATATTTTG 1395

RESULT 7

LOCUS T01235 359 bp mRNA EST 10-NOV-1992
DEFINITION WEST01956 Early embryo, Stratagene (cat. #937007) Caenorhabditis
elegans cDNA clone CEESO41, mRNA sequence.

ACCESSION

NID T01235

g277716

VERSION T01235.1 GI:277716

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 359)

REFERENCE McCombie,W.R., Kelley,J.M., Aubin,L., Goscoechea,M.,

AUTHORS FitzGerald,M.G., Wu,A., Adams,M.D., Dubnick,M., Kerlavage,A.R.,

Venter,J.C. and Fields,C.A.

Caenorhabditis elegans CDNAS

Unpublished (1993)

Other_ESTs: WEST01957

Contact: Kerlavage, AR

Bioinformatics

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Fax: 3018699423

Email: arkerlav@tigr.org

Seq primer: M13 Forward.

Location/Qualifiers

source

1. .359

/organism="Caenorhabditis elegans"

/db_xref="taxon:6239"

/clone="CEESO41"

/clone_lib="Early embryo, Stratagene (cat. #937007)"

115 a 61 c 60 g 122 t 1 others

BASE COUNT

ORIGIN

Query Match 0.4%; Score 31; DB 8; Length 359;

Best Local Similarity 100.0%; Pred. No. 2.09e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 TACAGTAGTCATTTAAAGGATTACTGTAGTT 52

||||| ||||| ||||| ||||| ||||| |||||

QY 1527 TACAGTAGTCATTTAAAGGATTACTGTAGTT 1557

RESULT 8

LOCUS C50455 360 bp mRNA EST 11-SEP-1997
DEFINITION C50455 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk483h7 5', mRNA sequence.

ACCESSION

NID C50455

g2387708

VERSION C50455.1 GI:2387708

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 360)

REFERENCE Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,

AUTHORS Sano,M., Miyata,A. and Nishigaki,A.

TITLE Expression map of the C.elegans genome

JOURNAL Unpublished (1996)

COMMENT On Sep 12, 1996 this sequence version replaced gi:1406982.

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FEATURES

source

1..360
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="CBI489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk483h7"
/clone_lib="Yuji Kohara unpublished cDNA"

BASE COUNT 115 a 60 c 68 g 117 t

ORIGIN

Query Match 0.4%; Score 28; DB 15; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.43e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 GTGCGCTTTAAGGAGTACTGTAATTC 126

|||||

Cp 5264 GTGCGCTTTAAGGAGTACTGTAATTC 5237

RESULT 9

LOCUS D75308 360 bp mRNA EST 14-DEC-1995
DEFINITION CELK098H4F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk98h4 5', mRNA sequence.

ACCESSION D75308

NID g1121092

VERSION D75308.1 GI:1121092

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)

AUTHORS Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
Tabara,H.

TITLE Toward an expression map of the C.elegans genome

JOURNAL

Unpublished (1994)

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Fax: 0559-75-6240

Email: ykohara@dbj.nig.ac.j

Insert Length: 895 Std Error: 0.00

High quality sequence stop: 363.

FEATURES

source

1..360
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="CBI489 him-8(e1489)"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
/db_xref="taxon:6239"
/clone="yk98h4"
/clone_lib="Yuji Kohara unpublished cDNA"

BASE COUNT 107 a 81 c 52 g 119 t

ORIGIN

Query Match 0.4%; Score 27; DB 32; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.01e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 GTCATTTAAGAATTACTGTAGTTTC 115

|||||

Cp 1437 GTCATTTAAGAATTACTGTAGTTTC 1411

RESULT 10

LOCUS B01439 66 bp DNA GSS 26-JUN-1996
DEFINITION CSRL-131f8-u CSRL flow sorted Chromosome 11 specific cosmid Homo
sapiens genomic clone CSRL-131f8, genomic survey sequence.

ACCESSION B01439

NID g1410717

VERSION B01439.1 GI:1410717

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 66)

AUTHORS

Evans,G.A., Burbee,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M.,
Jones,D., Ward,T., Gillilan,E., Schagemann,J., Probst,S.,
Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M.,
Kupfer,K. and Garner,H.R.

Genomic Sequence Sampled Map of Chromosome 11

JOURNAL

Unpublished (1996)

COMMENT

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Tel: 214-648-1600

Fax: 214-648-1666

Email: gevas@utsw.swmed.edu, shane@mcdermott.swmed.edu

Seq primer: T7

Class: cosmid ends

High quality sequence stop: 66.

FEATURES

source

1..66
Location/Qualifiers
/organism="Homo sapiens"
/note="Vector: sCos-1; Human Chromosome 11 specific cosmid
library prepared from flow sorted human Chromosome 11
derived from Chinese Hamster Ovary (CHO) monochromosomal
somatic cell hybrid, J1"
/db_xref="taxon:9606"
/clone="CSRL-131f8"
/clone_lib="CSRL flow sorted Chromosome 11 specific
cosmid"
/sex="female"
/cell_type="chimeric hamster somatic cell hybrid"
9 a 4 c 18 g 34 t 1 others

BASE COUNT

ORIGIN

Query Match 0.3%; Score 21; DB 37; Length 66;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 AGATGTGTGTGTGTGTGTG 28

|||||

Cp 2830 AGATGTGTGTGTGTGTG 2810

RESULT 11

LOCUS B36009 96 bp DNA GSS 16-OCT-1997
DEFINITION HS-1031-A2-H07-MR.abi CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate-CT 811 Col-14 Row-O, genomic survey
sequence.

ACCESSION B36009

NID g2535378

VERSION B36009.1 GI:2535378

KEYWORDS GSS.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 96)

AUTHORS

Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,

TITLE
JOURNAL
COMMENT

Tralcoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
Unpublished (1997)

Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT 811 row: O column: 14
Class: BAC ends
High quality sequence stop: 96.
Location/Qualifiers

FEATURES

source

1. .96
/organism="Homo sapiens"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"
/db_xref="taxon:9606"
/clone="Plate=CT 811 Col=14 Row=O"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"

BASE COUNT 16 a 16 c 32 g 32 t
ORIGIN

Query Match 0.3%; Score 21; DB 37; Length 96;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 TGTGTGTGTGTGTGTGTGACA 52
|||||
Cp 2827 TGTGTGTGTGTGTGTGTGACA 2807

RESULT 12
LOCUS AA084532 109 bp mRNA EST 02-FEB-1997
DEFINITION zf76c11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:382868 5', mRNA sequence.
ACCESSION AA084532
NID g1626588
VERSION AA084532.1 GI:1626588
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 109)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

On Apr 14, 1993 this sequence version replaced gi:692640.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 291 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham.

FEATURES

source

1. .109
/organism="Homo sapiens"
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCTGAAGTGGGAGCGCGCGCTTTTCTTTTCTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library constructed by Bento Soares
and M.Fatima Bonaldo.
/db_xref="GDB:1291125"
/db_xref="taxon:9606"
/clone="IMAGE:382868"
/clone_lib="Soares_pineal_gland_N3HPG"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT 33 a 25 c 17 g 33 t 1 others
ORIGIN

Query Match 0.3%; Score 20; DB 36; Length 109;
Best Local Similarity 95.2%; Pred. No. 1.19e-01;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 52 GNCACACACACACACACAT 72
|
Qy 2808 GTCACACACACACACACAT 2828

RESULT 13
LOCUS AA210472 122 bp mRNA EST 19-FEB-1997
DEFINITION mu30g03.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:640948 5',
mRNA sequence.
ACCESSION AA210472
NID g1807769
VERSION AA210472.1 GI:1807769
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 122)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)

TITLE
JOURNAL
COMMENT

On Sep 12, 1996 this sequence version replaced gi:1397488.

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WashU-HHMI Mouse EST Project
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:392940

Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 105.

FEATURES

source

Location/Qualifiers
1. .122
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
/db_xref="taxon:10090"

BASE COUNT 29 a 9 c 43 g 41 t
ORIGIN

/map="19"
/clone="IMAGE:640948"
/clone_lib="Soares 2NBMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"

Query Match 0.3%; Score 22; DB 9; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.90e-04;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 81 GAGATGTGTGTGTGTGTG 102
|||||
Cp 2831 GAGATGTGTGTGTGTGTG 2810

RESULT 14
LOCUS AQ308985 126 bp DNA GSS 21-DEC-1998
DEFINITION CITBI-E1-2525L8.TF CITBI-E1 Homo sapiens genomic clone 2525L8,
genomic survey sequence.
ACCESSION AQ308985
NID g4041019
VERSION AQ308985.1 GI:4041019
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 126)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.

TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CITBI-E1-2525L8.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES Location/Qualifiers
source 1..126
/organism="Homo sapiens"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
/db_xref="taxon:9606"
/clone="2525L8"
/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
BASE COUNT 37 a 6 c 48 g 35 t
ORIGIN

Query Match 0.3%; Score 21; DB 41; Length 126;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 42 TGTGTGTGTGTGTGTGACA 62
|||||
Cp 2827 TGTGTGTGTGTGTGTGACA 2807

RESULT 15

LOCUS AA067881 136 bp mRNA EST 06-FEB-1997
DEFINITION mm32f03.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:523229 5', mRNA sequence.

ACCESSION AA067881
NID g1566161
VERSION AA067881.1 GI:1566161
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 136)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Sep 12, 1996 this sequence version replaced gi:1394336.

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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Email: mouseest@watson.wustl.edu

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IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:317077

Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 128.
Location/Qualifiers

FEATURES source

1..136
/organism="Mus musculus"
/strain="C57BL/6"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
/db_xref="taxon:10090"
/clone="IMAGE:523229"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"

BASE COUNT 23 a 39 c 24 g 50 t
ORIGIN

Query Match 0.3%; Score 21; DB 35; Length 136;
Best Local Similarity 100.0%; Pred. No. 6.31e-03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 TGTGTGTGTGTGTGTGACA 38
|||||
Cp 2827 TGTGTGTGTGTGTGTGACA 2807

Search completed: Mon Aug 9 00:23:21 1999
Job time : 12755 secs.

